

F158-208/Domain: animal Kunitz-type proteinase inhibitor homology <BP>  
F136-86/45-69,61-82,96-149,106-130,122-145,158-208,167-191,183-204/Diulfide bonds: #src

Query Match 100.0%; Score 1306; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 3, 2e-110;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MDPARPLGSIILLPLTEALGDAAPGPGNNARICILPLPDVPGCALLLRYRDTQTS 60
DB 1 MDPARPLGSIILLPLTEALGDAAPGPGNNARICILPLPDVPGCALLLRYRDTQTS 60
QY 61 CROPLVGGCGGNANNFYTWBACDCAWRLEKVPKVCRLQVSDQCEGSTEKTFPFLSSM 120
DB 61 CROPLVGGCGGNANNFYTWBACDCAWRLEKVPKVCRLQVSDQCEGSTEKTFPFLSSM 120
QY 121 TCEKPFSGGCHRRIRIENRPDPATCMGFCAPKKIPEFCSPKDEGLCSANVTRYENPRY 180
DB 121 TCEKPFSGGCHRRIRIENRPDPATCMGFCAPKKIPEFCSPKDEGLCSANVTRYENPRY 180
QY 181 RTCDAPTYGCGGNDNNFVSREDCKRAKALKKKKMPRLAPASRIKIRKKQF 235
DB 181 RTCDAPTYGCGGNDNNFVSREDCKRAKALKKKKMPRLAPASRIKIRKKQF 235

```

## RESULT 2

146937  
tissue factor pathway inhibitor - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #ext\_change 09-Jul-2004

C/Accession: 146937

R/Belaouaj, A.; Kuppunawamy, M.N.; Birktoft, J.J.; Bajaj, S.P.

Thromb. Res. 69, 449-553, 1993

A/Title: Revised cDNA sequence of rabbit tissue factor pathway inhibitor.

A/Reference number: 146937; MUID:93276427; PMID:8503123

A/Accession: 146937

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-239 <BEL>

A/Cross-references: UNIPROT:P19761; UNIPARC:UPI000016C6D; GB:861902; NID:9386015; PIND:

C/Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor

F149-99/Domain: animal Kunitz-type proteinase inhibitor homology <BP11>

F120-170/Domain: animal Kunitz-type proteinase inhibitor homology <BP12>

F1212-262/Domain: animal Kunitz-type proteinase inhibitor homology <BP12>

Query Match 29.9%; Score 390; DB 2; Length 299;  
Best Local Similarity 30.8%; Pred. No. 1, 1e-27;

Matches 88; Conservative 30; Mismatches 78; Indels 90; Gaps 7;

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QY 12 LLLFLTEALGDAAPGPGNNARICILPLPDVPGCALLLRYRDTQ 59
DB 13 LLLGLVPAVSAAEDEFNTITDIKPIQKTHSCAMKVDGFCRAIYKGFPIILTH 72
QY 60 SCROPLVGGCGGNANNFYTWBACDCAWRLEKVPKVCRLQ 99
DB 73 QCEBFIYGGCGGNANNFYTWBACDCAWRLEKVPKVCRLQ 130
QY 100 VSDVQCEGSTEKTFPFLSSMTCCKEFGGCHRRIRIENRPDPATCMGFC 149
DB 131 -----GYTRFFYNQSKOCERKYGCGCLGNT--NNPESLSECKTNCENTPSDPOVD 180
QY 150 -----APKKI-----SPFCYSPKDEGLCSANVTRYENPRYRTCDAP 186
DB 181 DHRTQNTLVNNTLINTPTAPARRMAHGSWCLPDPDRDLQANETRRFYNAIIGKCRPF 240
QY 187 TTTGGGNDNNFVSREDCKRAKAL-----KKKKMP 219
DB 241 KISGGGNNNFTSKKACITACKKGFIRMLSKGGLIKTRKKKKQF 286

```

## RESULT 3

tissue factor pathway inhibitor precursor [validated] - human  
N/Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation inhib

C/Species: Homo sapiens (man)

C/Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #ext\_change 09-Jul-2004

C/Accession: A23712; A39176; A28650; A60433; B60433; S13034; A34315; A38294; S03903

R/Girard, T.J.; Eddy, R.; Weselohmdt, R.L.; Macphail, L.A.; Likert, K.M.; Byers, M.G.

J. Biol. Chem. 266, 5036-5041, 1991

A/Title: Structure of the human lipoprotein-associated coagulation inhibitor gene. Intro/

A/Reference number: A23712; MUID:91161593; PMID:2002445

A/Accession: A23712

A/Molecule type: DNA

A/Residues: 1-304 <GIR>

A/Cross-references: UNIPROT:P10646; UNIPARC:UPI0000136C9F; GB:M59493; GB:M59499; NID:9187

R/van der Logt, C.P.E.; Reijnders, P.H.; Bertina, R.M.

Biochemistry 30, 1571-1577, 1991

A/Title: Intron-exon organization of the human gene coding for the lipoprotein-associated

A/Reference number: A39176; MUID:91129227; PMID:1993173

A/Accession: A39176

A/Molecule type: DNA

A/Residues: 1-304 <VAN>

A/Cross-references: UNIPARC:UPI0000136C9F; GB:M58650; GB:J05312; NID:9186827; PIND:AAA594

R/Mun, T.C.; Kretzmer, K.K.; Girard, T.J.; Miletich, J.P.; Broze Jr., G.J.

J. Biol. Chem. 263, 6001-6004, 1988

A/Title: Cloning and characterization of a cDNA coding for the lipoprotein-associated co

A/Reference number: A28650; MUID:88198127; PMID:2452157

A/Accession: A28650

A/Molecule type: mRNA

A/Residues: 1-304 <MUN>

A/Cross-references: UNIPARC:UPI0000136C9F; GB:J03225; NID:9180545; PIND:AAA5202.1; PIND:

A/Note: Part of this sequence, including the amino end of the mature protein, was confir

R/Girard, T.J.; Warren, L.A.; Novotny, W.F.; Bejcek, B.E.; Miletich, J.P.; Broze Jr., G.J.

Thromb. Res. 55, 37-50, 1989

A/Title: Identification of the 1.4 KB and 4.0 KB messages for the lipoprotein associated

A/Reference number: A60433; MUID:89388722; PMID:2781520

A/Accession: A60433

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-304 <G12>

A/Cross-references: UNIPARC:UPI0000136C9F

A/Experimental source: endothelial cells

A/Accession: B60433

A/Molecule type: protein

A/Residues: 'XX', 31-53, 'X', 55-56 <G13>

A/Cross-references: UNIPARC:UPI0000173151

A/Experimental source: recombinant material from mouse C137 cells

A/Reference number: A34315; MUID:90036996; PMID:2553722

A/Accession: A34315

A/Molecule type: protein

A/Residues: 'XX', 31-33, 'L', 35-50 <NOV>

A/Cross-references: UNIPARC:UPI0000173152

R/Novotny, W.F.; Girard, T.J.; Miletich, J.P.; Broze Jr., G.J.

J. Biol. Chem. 264, 18832-18837, 1989

A/Title: Purification and characterization of the lipoprotein-associated coagulation inh

A/Reference number: A34315; MUID:90036996; PMID:2553722

A/Accession: A34315

A/Molecule type: protein

A/Residues: 'XX', 31-33, 'L', 35-50 <NOV>

A/Cross-references: UNIPARC:UPI0000173153

A/Experimental source: plasma

R/Pedersen, A.H.; Nordfang, O.; Norris, F.; Wiberg, F.C.; Christensen, P.M.; Moeller, K.F.

J. Biol. Chem. 265, 16786-16793, 1990

A/Title: Recombinant human extrinsic pathway inhibitor. Production, isolation, and charac

A/Reference number: A38294; MUID:91009092; PMID:2211593

A/Accession: A38294

A/Molecule type: protein

A/Residues: 29-41 <PED>

A/Cross-references: UNIPARC:UPI0000173154

R/Girard, T.J.; Warren, L.A.; Novotny, W.F.; Likert, K.M.; Brown, S.G.; Miletich, J.P.; E

Nature 338, 518-520, 1989

A/Title: Functional significance of the Kunitz-type inhibitory domains of lipoprotein-ase

A/Reference number: S03903; MUID:89181950; PMID:2927510

A/Contents: annotation; site-directed mutagenesis

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 9, 2006, 19:53:09 / Search time 40 Seconds  
(without alignments)  
565.273 Million cell updates/sec

Title: US-10-800-057-2

Perfect score: 1306  
Sequence: 1 MDPARPLGLSILLFLTEAA.....KKMPRLAPSRIRKIRKQF 235

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	1306	100.0	235	2 A54951 tissue factor path
2	390	29.9	299	2 I46937 tissue factor path
3	388	29.7	304	1 T1H0GK tissue factor path
4	384.5	29.4	304	1 JC2264 tissue factor path
5	376	28.8	302	1 T1RTGK tissue factor path
6	372.5	28.5	300	2 S12143 lipoprotein-associ
7	346.5	26.5	396	2 S53325 tissue factor path
8	305.5	23.4	2225	2 T26063 hypothetical prote
9	303	23.2	2167	2 T34395 hypothetical prote
10	299	22.9	1965	2 T33216 hypothetical prote
11	292.5	22.4	1558	2 C89114 protein C37C3.6a
12	285	21.8	922	2 T23573 hypothetical prote
13	279.5	21.4	1522	2 H88380 protein T22F7.3
14	271.5	20.8	1416	2 E88550 protein ZC64.1
15	271.5	20.8	2844	2 S28291 hypothetical prote
16	268	20.5	1474	2 D88550 protein ZC64.6
17	268	20.5	1599	2 T16210 hypothetical prote
18	253.5	19.4	1043	2 T19734 hypothetical prote
19	252	19.3	1743	2 T26659 hypothetical prote
20	240	18.4	1391	2 T20406 hypothetical prote
21	239	18.3	838	2 T20125 hypothetical prote
22	215	16.5	252	2 JG0185 hepatocyte growth
23	215	16.5	1208	2 T27822 hypothetical prote
24	214	16.4	352	1 T1B0B1 alpha-1-microglobu
25	206	15.8	1203	2 T21275 hypothetical prote
26	199	15.2	692	2 T32880 hypothetical prote
27	197	15.1	228	2 T20219 inter-alpha-trypsi
28	196	15.0	123	2 A29652 alpha-1-microglobu
29	191	14.6	337	1 T1PGB1

30	188	14.4	183	2	T28711	hypothetical prote
31	186	14.2	125	1	T1H0B1	alpha-1-microglobu
32	186	14.2	349	2	S21089	alpha-1-microglobu
33	184.5	14.1	349	2	S35708	gamma-1-microglobu
34	182.5	14.0	355	1	S22181	gamma-1-microglobu
35	180	13.8	352	1	HCHU	alpha-1-microglobu
36	178.5	13.7	502	2	T20130	hypothetical prote
37	174	13.3	61	1	T1V1T1	hypothetical prote
38	173	13.2	335	2	T32657	venom basic protei
39	172	13.2	62	2	S19327	venom basic protei
40	168	12.9	62	2	S07451	proteinase inhibit
41	166.5	12.7	372	2	UC2556	alpha-1-microglobu
42	165.5	12.7	110	1	T1T0R	basic proteinase
43	165	12.6	65	1	T1V1VC	venom basic protei
44	164	12.6	265	2	A53390	Kunitz-type protei
45	163	12.5	57	2	A59204	basic proteinase 1

#### ALIGNMENTS

RESULT 1  
A54951  
Tissue factor pathway inhibitor-2 precursor - human  
N:Alternate names: placental protein 5 (PP5)  
C:Species: Homo sapiens (man)  
C>Date: 31-May-1996 #sequence revision 31-May-1996 #text\_change 09-Jul-2004  
C:Accession: A54951; I55185; A34029; C34029; B34029  
R:Spencer, C.A.; Kissel, W.; Mathews, S.; Foster, D.C.  
P:Proc. Natl. Acad. Sci. U.S.A. 91, 3353-3357, 1994  
A>Title: Molecular cloning, expression, and partial characterization of a second human c  
A:Reference number: A54951; MUID:94211862; PMID:8159751  
A:Accession: A54951  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-235 <RES>  
A:Cross-references: UNIPROT:P48307; UNIPARC:UPI00000362E2; GB:I27624; NID:9441149; PIDN:  
A:Experimental source: placenta  
R:Myagi, Y.; Koshikawa, N.; Yasumitsu, H.; Miyagi, E.; Hirahara, F.; Aoki, I.; Mitsu, I  
J Biochem. 116, 939-942, 1994  
A>Title: cDNA cloning and mRNA expression of a serine proteinase inhibitor secreted by c  
A:Reference number: I55185; MUID:95204397; PMID:7896752  
A:Accession: I55185  
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBI  
A:Molecule type: mRNA  
A:Residues: 1-235 <RES>  
A:Cross-references: UNIPARC:UPI00000362E2; GB:I29992; NID:9484050; PIDN:BA06272.1; PID:  
A:Note: parts of this sequence, including the amino end of the mature protein, were deter  
R:Buterzow, R.; Huhale, M.L.; Bohm, H.; Vitraneu, I.; Seppelae, M.  
Biochem. Biophys. Res. Commun. 150, 483-490, 1988  
A>Title: Purification and characterization of placental protein 5.  
A:Reference number: A34029; MUID:88106628; PMID:3276312  
A:Accession: A34029  
A:Molecule type: protein  
A:Residues: 'A', 24-33, 'X', 35 <BU2>  
A:Cross-references: UNIPARC:UPI00001762A7  
A:Accession: C34029  
A:Molecule type: protein  
A:Residues: 47-50, 'X', 52-53 <BU2>  
A:Cross-references: UNIPARC:UPI00001762A7  
A:Accession: B34029  
A:Molecule type: protein  
A:Residues: 133, 'X', 135-137, 'X', 139-140, 'X', 142-144, 'X', 146 <BU3>  
A:Cross-references: UNIPARC:UPI00001762A7  
C:Genetics: GDB:TFPI2  
A:Gene: GDB:TFPI2  
A:Cross-references: GDB:354485  
C:Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor  
C:Keywords: anticoagulant; blood coagulation; duplication; glycoprotein; heparin binding;  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:23-235/Product: tissue factor pathway inhibitor-2 #status predicted <MAT>  
F:36-86/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>  
F:96-149/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>

C/Comment: The first Kunitz-type domain binds the factor VIIa/tissue factor complex; the C/Gene: GDB:127364; OMIM:153310  
 A/Gene: GDB:127364; OMIM:153310  
 A/Cross-references: GDB:127364; OMIM:153310  
 A/Map position: 2q32-2q33  
 A/Introns: 41/1, 107/1, 120/1, 179/1, 210/1, 270/1  
 C/Function: A/Description: regulates clotting by factor Xa-dependent inhibition of the coagulation cascade  
 A/Pathway: blood coagulation  
 C/Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor  
 C/Keywords: anticoagulant; blood coagulation; duplication; glycoprotein; heparin binding  
 F/1-28/Domain: signal sequence #status predicted <SIG>  
 F/29-304/Product: tissue factor pathway inhibitor #status experimental <MAT>  
 F/54-104/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>  
 F/125-175/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>  
 F/217-267/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>  
 F/284-289/Region: heparin binding #status predicted  
 F/30/Binding site: phosphate (Ser) (covalent) #status experimental  
 F/54-104, 63-87, 79-100, 125-175, 134-158, 150-171, 217-267, 226-250, 242-263/Dissulfide bonds: #  
 F/64/Inhibitory site: Lys (coagulation factor VII/tissue factor complex) #status experimental  
 F/145, 195, 256/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F/227/Inhibitory site: Arg (unidentified proteinase) #status predicted

Query Match 29.7%; Score 388; DB 1; Length 304;  
 Best Local Similarity 30.3%; Pred. No. 1.7e-27;  
 Matches 86; Conservative 37; Mismatches 85; Indels 76; Gaps 8;

QY 12 LLLFLTPALGDAAG-----PTGNNAICLLPLDYGCRALLLRYDRTY 58  
 DB 17 LLLFLTPALGDAAG-----PTGNNAICLLPLDYGCRALLLRYDRTY 76  
 QY 59 QSGROPLVGGCEGNNANFTWACDDACR-----IKKVKPCLQVSDQ-- 105  
 DB 77 RQCEBEPYGGCEGNNANFTWACDDACR-----IKKVKPCLQVSDQ-- 133  
 QY 106 CEGSTKYPFNLSMTCEKPSGCHNRLENPPDEATCGFC----- 149  
 DB 134 CRGYTRFYNNQTKQCEKPSGCHNRLENPPDEATCGFC----- 191  
 QY 150 -----APKKI-----PSPCYSPDDEGLCSANVTTRYFNPRTYTCDAFTYTCG 192  
 DB 192 NAYNNSLTPGSTKVPSPFEPHGSWCLTPADRGICANENRFFYNVSYGCRPFKSGCG 251  
 QY 193 GNDNFVSRBDCRACAKAL-----KKKKMPKLRFA 224  
 DB 252 GNDNFVSRBDCRACAKAL-----KKKKMPKLRFA 295

RESULT 4  
 UC2264  
 C/tissue factor pathway inhibitor precursor - rhesus macaque  
 N/Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation inhibi  
 C/Species: Macaca mulatta (rhesus macaque)  
 C/date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C/accession: UC2264  
 R/Name: S.; Kamakubo, Y.; Hamuro, T.; Fujimoto, H.; Ishihara, M.; Yonemura, H.; Miyamot  
 J. Biochem. 115, 708-714, 1994  
 A/Title: Amino acid sequence and inhibitory activity of rhesus monkey tissue factor path  
 A/reference number: UC2264; MUID:94375417; PMID:8089087  
 A/accession: J02264  
 A/molecule type: mRNA  
 A/residues: 1-304 <Rm>  
 A/cross-references: UNIPROT:Q28864; UNIPARC:UPI0000136C90; GB:S73337; NID:G685016; PIDN  
 A/experimental source: liver  
 C/Comment: This protein inhibits the activities of factor Xa and tissue factor-factor VI  
 C/superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor  
 C/Keywords: anticoagulant; glycoprotein; serine proteinase inhibitor  
 F/1-28/Domain: signal sequence #status predicted <SIG>  
 F/29-304/Product: tissue factor pathway inhibitor #status predicted <MAT>  
 F/54-104/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>  
 F/125-175/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>  
 F/217-267/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>

F/54-104, 63-87, 79-100, 125-175, 134-158, 150-171, 217-267, 226-250, 242-263/Dissulfide bonds: #  
 F/64/Inhibitory site: Lys (coagulation factor VII/tissue factor complex) #status predicted  
 F/145, 195, 256/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F/227/Inhibitory site: Arg (unidentified proteinase) #status predicted

Query Match 29.4%; Score 384.5; DB 1; Length 304;  
 Best Local Similarity 30.7%; Pred. No. 3.5e-27;  
 Matches 91; Conservative 37; Mismatches 91; Indels 77; Gaps 10;

QY 1 MDAPAPGLST-LLFLTPALGDAAG-----PTGNNAICLLPLDYGCR 46  
 DB 5 MCKVHALWVSICLMTLAPAPLADNSDEDEBTITDTLPLKLMHSFCARPDGPK 64  
 QY 47 ALLAYYDRYQSGROPLVGGCEGNNANFTWACDDACR-----IKKVKP 95  
 DB 65 ALMKRFFPFIYRQCEBEPYGGCEGNNANFTWACDDACR-----IKKVKP 124  
 QY 96 CRLQVSDQ--CEGSTKYPFNLSMTCEKPSGCHNRLENPPDEATCGFC----- 149  
 DB 125 CRLQVSDQ--CEGSTKYPFNLSMTCEKPSGCHNRLENPPDEATCGFC----- 179  
 QY 150 -----APK-KIPSP-----CYSPDDEGLCSANVTTRYFNPRTY 180  
 DB 180 NGFYVDNYGTOLNAYNNSQTPSTKVPSPFEPHGSWCLTPADRGICANENRFFYNVSY 239  
 QY 181 RQCEBEPYGGCEGNNANFTWACDDACR-----IKKVKPCLQVSDQ-- 224  
 DB 240 GRCRPFKYSQCGNNANFTWACDDACR-----IKKVKPCLQVSDQ-- 295

RESULT 5  
 T1RTK  
 C/tissue factor pathway inhibitor precursor - rat  
 N/Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation inhibi  
 C/Species: Rattus norvegicus (Norway rat)  
 C/date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
 C/accession: JX0213  
 R/Name: J.; Eml, M.; Mukai, T.; Kato, H.  
 J. Biochem. 111, 681-687, 1992  
 A/Title: cDNA cloning and expression of rat tissue factor pathway inhibitor (TFPI).  
 A/reference number: JX0213; MUID:92348361; PMID:1639767  
 A/accession: JX0213  
 A/molecule type: mRNA  
 A/residues: 1-302 <Rm>  
 A/cross-references: UNIPROT:Q02445; UNIPARC:UPI0000136C92; DDBJ:D10926; NID:9220916; PIDN  
 A/experimental source: liver  
 C/Comment: This serine proteinase inhibitor regulates clotting by factor Xa-dependent int  
 C/superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor  
 C/Keywords: anticoagulant; blood coagulation; duplication; glycoprotein; heparin binding;  
 F/1-28/Domain: signal sequence #status predicted <SIG>  
 F/29-302/Product: tissue factor pathway inhibitor #status predicted <MAT>  
 F/53-103/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>  
 F/124-174/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>  
 F/222-272/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>  
 F/288-291/Region: heparin binding #status predicted  
 F/53-103, 62-86, 78-99, 124-174, 133-157, 145-170, 222-272, 231-255, 247-268/Dissulfide bonds: #st  
 F/63/Inhibitory site: Lys (coagulation factor VII/tissue factor complex) #status predicted  
 F/134/Inhibitory site: Arg (coagulation factor X) #status predicted  
 F/144, 251, 261/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F/232/Inhibitory site: Lys (unidentified proteinase) #status predicted

Query Match 28.8%; Score 376; DB 1; Length 302;  
 Best Local Similarity 33.1%; Pred. No. 2e-26;  
 Matches 84; Conservative 27; Mismatches 76; Indels 67; Gaps 9;

QY 36 CULPLDYGCRALLLRYDRTYQSGROPLVGGCEGNNANFTWACDDAC----- 86  
 DB 53 CMKADEGCKAMIRBYTPMNSHQBEPYGGCEGNNANFTWACDDAC----- 112  
 QY 87 ---WRLEKVPKVCRLQVSDQ--CEGSTKYPFNLSMTCEKPSGCHNRLENPPD 141

Db 113 KTTSGABK-PDFCFLE---EDPGICGFMTRYFNNOSSKCEQFKYGGCLGN--SNNFET 166  
QY 142 EATCMGFC-----APKKI-----PSFCYSPE 162  
Db 167 LEECRATCEBPVNEVOKGVYNTQITVTRDTVNVNVIPQATAPQGMWDGSCLEBPA 226  
QY 163 DEELGSANVTRYFNPRTYRTCDAPTTGGCGDNPNFVSREDCRACAK-ALKKKKKMPKL 221  
Db 227 DSELGCASEKRFYFNPAIGKCRQFNYTGGCGNNNNFTTKDCNRACKKSSKSSKRAK- 285  
QY 222 RFASRIKIRKKQ 235  
Db 286 -----TQRRKRSF 293

## RESULT 6

S12143

lipoprotein-associated coagulation inhibitor precursor - rabbit

N/Alternate names: endothelial cell coagulation inhibitor; endothelial cell tissue factor

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 16-Jul-1999

C/Accession: S12143; A61373

R/Nucleic Acid: Res. 18, 6440, 1990

A/Title: CDNA sequence of rabbit lipoprotein-associated coagulation inhibitor.

A/Reference number: S12143; M01D:91057146; PMID:2136251

A/Accession: S12143

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-300 &lt;RES&gt;

A/Cross-references: UNIPARC:UPI000016C583; EMBL:X54708; NID:G1612; PIDN:CAA38515.1; PID:

R/Colburn, P.; Crabo, J.W.; Buonasisti, V.

J. Cell. Physiol. 148, 320-326, 1991

A/Title: Enhanced inhibition of tissue factor by the extended form of an endothelial cell

A/Accession: A61373

A/Molecule type: protein

A/Residues: 25-33, 'X', '35-46 &lt;COL&gt;

A/Cross-references: UNIPARC:UPI0000176246

C/Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor

C/Keywords: anticoagulant; glycoprotein

F/51-100/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP1&gt;

F/121-171/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP2&gt;

F/113-263/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP3&gt;

Query Match 28.5%; Score 372.5; DB 2; Length 300;

Best Local Similarity 29.7%; Pred. No. 4.2e-26;

Matches 86; Conservative 32; Mismatches 75; Indels 97; Gaps 8;

QY 12 LILFLTBALGDAAG-----PTGNNABICLLPLDYGFCRALLRLYYD 55  
Db 13 LILGLVPAVSSAAEEDSEFTNTIDIKPLQKPTH8---FCAMKVVDDGFCRAVYIKRFFPN 69  
QY 56 RYTQSGROPLYGSGCEGNANNTFYWEACDDACWR-----IEKVPKY 95  
Db 70 ILAHOCEBFTYGGCEBENRFBSELECKKCAADYKMTTKLTFQKGDPCFLERDEPQI 129  
QY 96 CRLQVSVDDQCEGSTEKTEYFNLSSMTCEKFPFGGCHRNRIENRPPDEATCMGFC----- 149  
Db 130 CR-----GYTRFYFNNOSSKCEKFKYGGCLGN--NNFSELECKKNTCEPTSD 177  
QY 150 -----APKKI-----PSFCYSPEBGLGSANVTRYFNPRT 182  
Db 178 FQVDDHRTQTLNTVNTLINOPTAPARRMAFHGFWCLPRAEGLCOANIRFFVYALIGK 237  
QY 183 CAAPTYTGGGNDNNFVSREDCRACAKL-----KKKKKMP 219  
Db 238 CRPFKYSGGCGNNFTSKKACTTACKGPIPKSIGLITKRRKKQ 287

## RESULT 7

S53325  
tissue factor pathway inhibitor - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)  
C/Date: 01-Aug-1995 #sequence\_revision 01-Sep-1995 #text\_change 17-Mar-2003  
C/Accession: S53325  
R/Gillard, T.J.; Gallant, D.; Broze Jr., G.J.  
Biochem. J. 303, 923-928, 1994  
A/Title: Complementary DNA sequencing of canine tissue factor pathway inhibitor reveals  
A/Reference number: S53325; M01D:95071310; PMID:7980463  
A/Accession: S53325  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-396 <GIR>

A/Cross-references: UNIPARC:UPI00000878B3

C/Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor

C/Keywords: serine proteinase inhibitor

F/53-103/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP1&gt;

F/125-175/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP2&gt;

F/309-359/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP3&gt;

Query Match 26.5%; Score 346.5; DB 2; Length 396;

Best Local Similarity 24.6%; Pred. No. 1.2e-23;

Matches 92; Conservative 35; Mismatches 88; Indels 159; Gaps 10;

QY 12 LILFLTBALG---DAQEPFGNNAE-----CLPLDYGFCRALLRLYYDRTQ 59  
Db 17 LILNCASAPLNAVDESEBEPITDELPLRLHSFCALKUNGFCRAMIRYFFNIHQ 76  
QY 60 SCROFLYGSGCEGNANNTFYWEACDDACWRI-----EKY---PKVCLQVVDQ-- 105  
Db 77 QCEBFTYGGCEGNQNRFBSELECKKCAADYKMTTKLTFQKGDPCFLERDEPQI 133  
QY 106 CEGSTEKTEYFNLSSMTCEKFPFGGCHRNRIENRPPDEATCMGFC----- 149  
Db 134 CNGFTVRYNNVNSKCEGFKYGGCLGNL--NNFTLEQCKKNTCSIDLMDFTVNTG 191  
QY 150 ----- 149  
Db 192 SPGSMNNTSLFNSGDSLLPADSGDSMPDSEIGLQHDSESGGLQHDSESG 251  
QY 150 -----APKKI-----PSFCYS 160  
Db 250 GLQHDSESGGLQHDSESGGLQHDSDNTSPVSVNNDSTPRPPVYSSFLFPGSWCLT 311  
QY 161 PDEBGLGSANVTRYFNPRTYRTCDAPTTGGCGDNPNFVSREDCRACAKALKKKKKMPK 220  
Db 312 PADRGICHANESRFYFNPAIGKCRQFNYTGGCGNNNNFTSKKACTTACKGPIPKSIGLITKRRKKQ 371  
QY 221 LRFASRIKIRKKQ 234  
Db 372 L---IKTKRRKKQ 382

## RESULT 8

T26063

hypothetical protein w01f3.3 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C/Accession: T26063

R/Cummings, P.

submitted to the EMBL Data Library, March 1997

A/Reference number: Z20145

A/Accession: T26063

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-2225 &lt;WIL&gt;

A/Cross-references: UNIPROT:O45881; UNIPARC:UPI00000816RC; EMBL:Z292815; PIDN:CA07294.1;

A/Experimental source: clone w01f3

C/Genetics:

A/Map position: 5

A/Introns: 33/1, 56/1, 100/1, 142/3, 271/3, 451/1, 525/3, 774/1, 1093/1, 1178/1, 1221/1;

Query Match 23.4%; Score 305.5; DB 2; Length 2225;

Best Local Similarity 33.7%; Pred. No. 3.1e-19;



[illegible]

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RESULT 9
T34395
hypothetical protein C37C3.6b - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C/Accession: T34395; T34394
R/Gisrael, C.; Bradshaw, H.
submitted to the EMBL Data Library, July 1996
A/Description: The sequence of C. elegans coemid C37C3.
A/Reference number: 221518
A/Accession: T34395
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 12167 <GB>
A/Cross-references: UNIPROT:O76840; UNIPARC:UPI000007D957; EMBL:U64857; PIDD:AA25868.1
A/Experimental source: strain Bristol N2; clone C37C3
A/Accession: T34394
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 11555, 'SKP', <GB>
A/Cross-references: UNIPARC:UPI0000085C9F; EMBL:U64857; PIDD:AA25867.1; GSPDB:GN00023;
C/Genetic:
A/Gene: CESP:C37C3.6b; CESP:C37C3.6a
A/Map position: 5
A/Introns: 32/3; 104/2; 156/2; 207/1; 459/2; 536/3; 577/2; 1105/3; 1367/1; 1438/1; 1556/1
Query Match 23.2%; Score 303; DB 2; Length 2167;
Beat Local Similarity 32.3%; Pred. No. 5.1e-19;
Matches 64; Conservative 35; Mismatches 91; Indels 8; Gaps 4;
QY 29 TGNNAICLLPLDYPCCALILRIYYDRYTSQROFLYGCAGCGNANFYTWACDDACR 88
DB 1724 TGAPELCLMLPEGRSGCYNDILRMFPDSKSGCVTFMWSGCGNPNHFTSQETCERACGX 1783
QY 89 IEKPVKVCRLQVSVDQCEGSTEKYPNLSMTCKEFPSCGCHRRIRIENRPDEATCMGF 148
DB 1784 WRNV-AYVELPAEHGD-QOLAPRWYHDPKTSQCCMMWYGGGN--GNAFSSKADCESL 1839
QY 149 CAPKTIPI-----FCYSPKDEGLCSANVTRYFNPRYRTCDATFYTGCGGNDNPFVSRDC 204
DB 1840 CRVELTMSNNTDFCTLESAGACTISIMWTFDSTHLDCKPTTYGGCKGNQNRVFSKQC 1899
QY 205 KRAKAKALKKKKKMPKLR 222
DB 1900 QQSGCRPGDKTSBEDICTLR 1917
RESULT 10
T33216
hypothetical protein T07H8.4 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C/Accession: T33216

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R.Gattung, S.; Maggi, L.  
submitted to the EMBL Data Library, May 1998  
A.Description: The sequence of C. elegans cosmid T07H8.  
A.Reference number: 221303  
A.Accession: T33216  
A.Status: preliminary; translated from GB/EMBL/DBJ  
A.Molecule type: DNA  
A.Residues: 1-1965 <GAT>  
A.Cross-references: UNIPARC:UPI000017B37E; EMBL:AF067945; PIDDN:AACT68.1; GSPDB:GN00023  
A.Experimental source: strain Bristol N2; Clone T07H8  
C.Genetics8:  
A.Gene: GSP:T07H8.4  
A.Map position: 5  
A.Introns: 47/3; 77/2; 160/3; 198/1; 263/2; 315/1; 386/1; 620/3; 662/1; 706/1; 753/3; 886/1  
Query Match 22.9%; Score 299; DB 2; Length 1965;  
Best Local Similarity 30.0%; Pred. No. 1, 1e-18;  
Matches 84; Conservative 24; Mismatches 80; Indels 92; Gaps 12;

QY	31	NNAAI-CLLP--LDYGGPRALL-----	RYYYDYTSCHQPLVGS-EGGANNPFYWEAC	82
Db	1584	NEARVADCLPMHIGYGNKDESCLEPQAGFRFFYYDDANYGKCSQMWTYAGCGGANNPFYSYEIC		1643
QY	83	DDACRIERKVPK-----VC-----		96
Db	1644	QRTCSQSD--VPRLEIRKTRASSFEVCFBPEDRGICGNKSSTNPIKMTYGNQKCTSTFYS		1702
QY	97	-----RLQSVSDQCE-----	-----GSTEK-----YFNLISMTCKEFP	126
Db	1703	GGCGNRNRFAQDICTCNGTNGNMMNSNDPISFSPDWGSCNQGLAYWPFYNLTRETCDQFL		1762
QY	127	SGGCHRNRIENRPDEATCMGFCAPKKI	PSFCYSPKDEG-ICSANVTIRYTFNPRYTCDA	185
Db	1763	YGGCGGN--PARRPTFRIQKACACVTGTDP--CMESLIRGWSCEMSNRYYFNKRAKOCKG		1819
QY	186	PTYTGCGGNDNNPFVSRDCKRAKAKALKK---	KKEMPTLR	222
Db	1820	PHYTGGCGSGNNFLKESCOYTKCEKRPFRAPASKKKAKLK		1859

RESULT 11  
C89114  
protein C37C3.6a [imported] - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C/Accession: C89114  
R/Anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biology  
A/Reference number: AF5000; M01D;99069613; PMID:9851916  
A/Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.elegans/  
A/Note: published errata appeared in Science 283, 35, 1999; and  
A/Accession: C89114  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-1558 <STO>  
A/Cross-references: UNIPROT:Q81710; UNIPARC:UPI0000085C9F; GB:chr\_V; PIDN:AAC35867.1; PIR:G10000; PIR:G10000  
C/Genetics:  
A/Gene: C37C3.6a  
A/Map position: 5

[illegible]

Qy 141 DEATCMGFCAPKIPSPGSGKDEGLCSANVTRYENPRRTCDAPTYTGGGNNFVS 200  
 Db 1489 NEQCCRAACQNHK-DACQIPKVOGPGSGKSHYTYNTASHQCTFTYGGCLGNTNRFAT 1546  
 Qy 201 REDCKRAC 208  
 Db 1547 IEECQARC 1554

RESULT 12

hypothetical protein K10D3.4 - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C/Accession: T23573

R/Murray, A.  
 submitted to the EMBL Data Library, June 1996  
 A/Reference number: Z19762  
 A/Accession: T23573  
 A/Status: preliminary; translated from GB/EMBL/DBD  
 A/Molecule type: DNA  
 A/Residues: 1-922 <MIL>  
 A/Cross-references: UNIPROT:Q21418, UNIPARC:UP10000762C2, EMBL:Z75545, PIDN:CAA9886.1;  
 A/Experimental source: clone K10D3  
 C/Genetics:  
 A/Gene: CESP:K10D3.4  
 A/Map position: 1 228/1; 278/1; 355/1; 743/1; 802/1; 885/2  
 A/Intons: 60/1; 228/1; 278/1; 355/1; 743/1; 802/1; 885/2

Query Match 21.8%; Score 285; DB 2; Length 922;  
 Best Local Similarity 21.9%; Pred. No. 9.2e-18;  
 Matches 60; Conservative 36; Mismatches 76; Indels 102; Gaps 5;

Qy 35 ICLLPDYPCRALLRYYDRYTOSCRQFLYGGCGNANNFYTWACDCAKRIKVPK 94  
 Db 410 VCKLPREGQNCCTYSNRMWFNATGNCBERIYSGCGNANFETYKCCDYCDARSEFQ 469  
 Qy 95 -----VCRLOVSVDQC 106  
 Db 470 CIOGTALTDNSNGNFIICGSSASATTCPRANHYTYTGTYGCCPTQATYCSLSYSGASC 529  
 Qy 107 EGSTERYFNLSMTCEKFPSSGCHNRRIENRPPDEATCMGFCAPKIPSPGSGK 156  
 Db 530 GVAVTWYDSTRTCTQTSFNGCCDN--SNPATQDDCKDQCRVNSCDDGGEVWKEONG 587  
 Qy 157 -----FCYSPDDEGL-CSA-NVTRY 174  
 Db 588 AARACTNRCPSRTHYCTPVTTGTYQTSLACPSKNFVCSQPRDVGVRCSSTRISRW 647  
 Qy 175 YFNPRYRTCDAPTYTGGGNNFVSREDCKRAC 208  
 Db 648 YFNADSKTCQTEHYNGCBGRNRFASQKSCQNYC 681

RESULT 13

H88380  
 protein T22F7.3 [imported] - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001  
 C/Accession: H88380  
 R/anonymous, The C. elegans Sequencing Consortium.  
 Science 282, 2012-2018, 1998

A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biology  
 A/Reference number: A75000; MUID:99069613; PMID:9851916  
 A/Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_eleg  
 A/Accession: H88380  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-1522 <STO>  
 A/Cross-references: UNIPARC:UP1000017ASB5; GB:chr\_III; PIDN:AAA20672.1; PID:9529714; GSF  
 A/Note: highly similar to ZC84.1  
 C/Genetics:

A/Gene: T22F7.3  
 A/Map position: 3  
 Query Match 21.4%; Score 279.5; DB 2; Length 1522;  
 Best Local Similarity 26.0%; Pred. No. 4.7e-17;  
 Matches 73; Conservative 21; Mismatches 86; Indels 101; Gaps 8;

Qy 28 PTGNNAEICLLPDIYPCRALLRYYDRYTOSCRQFLYGGCGNANNFYTWACDCAK 87  
 Db 527 PTAQS--LCTQFRLDCTSAVRWYMYNATRSCEMFQYTGCGGNNFVTLMAQCKR 584  
 Qy 88 RLEKVPK-----VCRLOV 100  
 Db 585 GHVEPKCGHGAFRDRNGNFOQSDKQNGKPCPVNYVCSFDGTTGCCPTKAFQSLNP 644  
 Qy 101 SYDDQC-EGSTERYFNLSMTCEKFPSSGCHNRRIENRPPDEATCMGFCAPCA----- 150  
 Db 645 DKGVOGSGRSRYRYNSKQSCSEIYQYGCQGN--ANNFLSBDQHYCGVGCGPENG 702  
 Qy 151 -----PKIPSP-----FCYSPDDEGL-CSA-AN 170  
 Db 703 PLRDEATNRMSCSEQKSCPTHECLTIPVNGHVSRCPTQKHICSGPPOGNNHCKS 762  
 Qy 171 VTRYYNPRYRTCDAPTYTGGGNNFVSREDCKRACAKA 211  
 Db 763 VGRFYNIIVTRCATFYNGCNGNINFAQSECNNPCSSA 803

RESULT 14

H88550  
 protein ZC84.1 [imported] - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
 C/Accession: E88550  
 R/anonymous, The C. elegans Sequencing Consortium.  
 Science 282, 2012-2018, 1998

A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biology  
 A/Reference number: A75000; MUID:99069613; PMID:9851916  
 A/Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_eleg  
 A/Accession: E88550  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-1416 <STO>  
 A/Cross-references: UNIPROT:O03610, UNIPARC:UP1000013BAA7; GB:chr\_III; PIDN:CAA79569.1; I  
 A/Note: similar to Serine protease inhibitor, Kunitz type  
 C/Genetics:  
 A/Gene: ZC84.1  
 A/Map position: 3

Query Match 20.8%; Score 271.5; DB 2; Length 1416;  
 Best Local Similarity 24.5%; Pred. No. 2.3e-16;  
 Matches 74; Conservative 25; Mismatches 86; Indels 117; Gaps 8;

Qy 21 LGDAQERTGNAR-----ICLLPDIYPCRALLRYYDRYTOS 60  
 Db 400 IGEBAQR--CONNAQCPSSHECKADQVCCPRKQTCAQPLRIGDCTENVKRYMYNARTQ 458  
 Qy 61 CROFLYGGCGNANNFYTWACDCAKRIKVPK----- 94  
 Db 459 COMPEYTCGQNDNPFDSIMCQNFCKRAIEPKICQOAYKDMGNTVTGSGNGCCPAN 518  
 Qy 95 -----VCRLOVSVDQC-EGSTERYFNLSMTCEKFPSSGCHNRRI 135  
 Db 519 YECYFDGSGQMCPTKAPFAGSLNDSGIQAGAGSFYKXYNPQTNGCSFOYNGCDGN-- 576  
 Qy 136 ENRPDARTCMGFCAPKIPSPGSGK----- 156  
 Db 577 SNNFANRDCASYGVGCGFNGGTPPLADHSGWVWGAQOTSCEPDSHCIPVLVGNLSLN 636  
 Qy 157 -----FCYSPDDEGL-CSAN-VTRYENPRYRTCDAPTYTGGGNNFVSREDCKR 206  
 Db 637 RCCEPRAMCGLPFGQGTGCGANVYGRYFIVISQCTSPFGGCGGNNANFLNIQCKN 696

QY 207 AC 208  
DB 697 FC 698

## RESULT 15

828291 hypothetical protein ZC84.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C&gt;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004

C/Accession: 828291

R:Thomas, K.

Submitted to the EMBL Data Library, December 1992

A/Reference number: 828285

A/Accession: 828291

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-2844 &lt;THO&gt;

A/Cross-references: UNIPROT:Q03610; UNIPARC:UPI000017BCB9; EMBL:Z19157

C/Genetics: A/Introns: 14/1; 32/3; 57/1; 192/3; 277/1; 398/1; 439/1; 474/1; 497/1; 813/1; 1135/1; 12

493/1; 2555/1; 2720/1; 2739/3; 2819/1

F/220-274/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP11&gt;

F/343-395/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP12&gt;

F/442-492/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP13&gt;

F/546-598/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP14&gt;

F/654-706/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP15&gt;

F/1662-1716/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP16&gt;

F/1787-1839/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP17&gt;

F/1845-1895/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP18&gt;

F/1952-2004/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP19&gt;

F/2097-2152/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP10&gt;

Query Match 20.8%; Score 271.5; DB 2; Length 2844;

Best local similarity 24.5%; Pred. No. 4.5e-16;

Matches 74; Conservative 25; Mismatches 86; Indels 117; Gaps 8;

QY 21 LGDAQEPFGNNAE-----ICLLPLDYGPCRALILRYTYDRYQS 60  
DB 408 IGBEAQR-CQNNACPSHSECKADQGVCCPRKQITCAQPLRIGDCTENVKRYNNATRQ 466  
QY 61 CRQFLYGGCGEGNANFTWAEACDCAWRIKVPK----- 94  
DB 467 CQMFETYGCGNDNPFDSIMDCQNFCKNAIPBPKICQQAQYKDMFGNFTCSNGMCCPAN 526  
QY 95 -----VCRLQVSVDDQC-EGSTERYFPNLSMTCEKFPSSGCHRRRI 135  
DB 527 YECYPDGSGMCCPTKAFYTSLSMTDSGIQCGAGSTFKYYINPQGNCESPQYNGCDGN-- 584  
QY 136 ENRPDEATCMGFCAPKRIPS----- 156  
DB 585 SNNFANRDACESYCSVGGCPNGGTPLADHSGMWVCGAQGTCPSDHECIPVLWGNSLIN 644  
QY 157 -----PCYSPDEGL-CSAN-VTRYYPNRYRTCDATYTGCGGNDNPFVSRBCKR 206  
DB 645 RCCEPRAVMGLPQGGTQCGANVQRYNYITVSQCTSPQGGCDGNANFNLTQQCRN 704  
QY 207 AC 208  
DB 705 FC 706

Search completed: March 9, 2006, 19:57:33  
Job time: 42 sec

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using SW model

Run on: March 9, 2006, 19:49:49 ; Search time 230 Seconds

(without alignments)  
720.866 Million cell updates/sec

Title: US-10-800-057-2

Perfect score: 1306

Sequence: 1 MDPARPLGSLILPLITLTA.....KMPKLRFAIRIRIKRQKP 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

# SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	1306	100.0	235	1 TPPI2_HUMAN	P48307 homo sapien
2	1306	100.0	235	2 O6ME8_HUMAN	O6ME8 homo sapien
3	1231.5	94.3	224	2 O8NAK6_HUMAN	O8NAK6 homo sapien
4	94.3	72.2	167	2 O8NE89_HUMAN	O8NE89 homo sapien
5	93.9	71.9	234	2 O7YRQ8_BOVIN	O7YRQ8 bos taurus
6	65.4	50.1	230	2 O8CF99_RAT	O8CF99 rattus norv
7	64.4	49.3	230	1 TPPI2_MOUSE	O35536 mus musculu
8	63.5	48.6	224	2 O7T0Z5_XENLA	O7T0Z5 xenopus lae
9	63.0	48.2	219	2 O5FYV6_XENTR	O5FYV6 xenopus tro
10	45.8	35.1	190	2 O4RDL7_TETNG	O4RDL7 tetraodon n
11	39.6	30.3	304	2 O5RFP8_PONPY	O5RFP8 pongo pygma
12	38.8	29.7	304	1 TPPI1_HUMAN	P10646 homo sapien
13	38.8	29.7	304	2 O5JTS4_HUMAN	O5JTS4 homo sapien
14	38.7	29.7	300	1 TPPI1_RABIT	P19761 coryctolagus
15	38.7	29.6	287	2 O93424_CYPCA	O93424 cyprinus ca
16	38.4	29.4	304	1 TPPI1_MACMU	O28864 macaca mula
17	37.8	28.9	306	1 TPPI1_MOUSE	O54819 mus musculu
18	37.6	28.8	302	1 TPPI1_RAT	O02445 rattus norv
19	367.5	28.1	279	2 O7Z242_BRABR	O7Z242 brachydanio
20	367.5	28.1	292	2 O5O4K2_BRABR	O5O4K2 brachydanio
21	361	27.6	241	2 O7FXZ1_AMOCA	O7FXZ1 anopheles g
22	358.5	27.5	759	2 O8IT91_AMOCA	O8IT91 ancylostoma
23	357.5	27.4	3198	2 O9UG88_MANSE	O9UG88 manduca sex
24	346.5	26.5	396	2 O28874_CANPA	O28874 canis famli
25	336.5	25.8	2772	2 O9VAV4_DROME	O9VAV4 drosophila
26	336.5	25.8	2776	2 O863A0_DROME	O863A0 drosophila
27	336.5	25.8	2894	2 O7KKX2_DROME	O7KKX2 drosophila
28	336.5	25.8	2898	2 O86829_DROME	O86829 drosophila
29	331.5	25.4	419	2 O4SB60_TETNG	O4SB60 tetraodon n
30	325	24.9	1572	2 O44938_HAECCO	O44938 haemochnus
31	310.5	23.8	2163	2 O61TS1_CABER	O61TS1 caenorhabd1

32	310.5	23.8	2174	2 O9G0R0_DROME	O9G0R0 drosophila
33	305.5	23.4	2325	2 O45881_CABER	O45881 caenorhabd1
34	305	23.4	1487	2 O8MPV5_CABER	O8MPV5 caenorhabd1
35	303	23.2	2167	2 O76840_CABER	O76840 caenorhabd1
36	301	23.0	2157	2 O60197_CABER	O60197 caenorhabd1
37	300	23.0	1604	2 O5Z835_CABER	O5Z835 caenorhabd1
38	300	23.0	1818	2 O5Z836_CABER	O5Z836 caenorhabd1
39	300	23.0	1954	2 O5Z837_CABER	O5Z837 caenorhabd1
40	300	23.0	1995	2 O5Z839_CABER	O5Z839 caenorhabd1
41	300	23.0	2006	2 O5Z840_CABER	O5Z840 caenorhabd1
42	300	23.0	2007	2 O5Z842_CABER	O5Z842 caenorhabd1
43	295.5	22.6	1979	2 O60WPI_CABER	O60WPI caenorhabd1
44	292.5	22.4	1558	2 O81710_CABER	O81710 caenorhabd1
45	285	21.8	568	2 O60Q68_CABER	O60Q68 caenorhabd1

## ALIGNMENTS

RESULT 1  
ID TPPI2\_HUMAN STANDARD; PRT; 235 AA.  
AC P48307;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Tissue factor pathway inhibitor 2 precursor (TPPI-2) (Placental  
protein 5) (Pfs).  
GN Name=TPPI2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.  
RC TISSUE=Placenta;  
RX MEDLINE=95204397; PubMed=7896752;  
RA Miyagi Y., Koshikawa N., Yasumitsu H., Miyagi E., Hirahara F.,  
Aoki I., Misugi K., Umeda M., Miyazaki K.;  
RT "cDNA cloning and mRNA expression of a serine proteinase inhibitor  
secreted by cancer cells: identification as placental protein 5 and  
tissue factor pathway inhibitor-2.";  
RL J. Biochem. 116:939-942(1994).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Placenta;  
RX MEDLINE=94211862; PubMed=8159751;  
RA Sprecher C.A., Kissel W., Mathewes S., Foster D.C.;  
RT "Molecular cloning, expression, and partial characterization of a  
second human tissue-factor-pathway inhibitor.";  
RL Proc. Natl. Acad. Sci. U.S.A. 91:3353-3357(1994).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RA Maggi L.;  
RT Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=12477932; PubMed=11342222; DOI=10.1016/S0167-4781(00)00288-0;  
RA Kamei S., Kazama Y., Kujiiper J.L., Foster D.C., Kissel W.;  
RT "Genomic structure and promoter activity of the human tissue factor  
pathway inhibitor-2 gene.";  
RL Biochim. Biophys. Acta 1517:430-435(2001).  
RN [5]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Krausner R.D., Collins F.S., Wagner L., Schemm C.M., Schaller G.D.,  
Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Vallalon D.K., Munzy D.M., Sodergren B.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton B., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Snevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN PARTIAL PROTEIN SEQUENCE OF 23-35; 47-53 AND 133-146.  
RP TISSUE=Placenta;  
RX MEDLINE=88106628; PubMed=3276312;  
RA Buerzow R., Huhtala M.-L., Bohn H., Virtanen I., Seppaelae M.;  
RT Purification and characterization of placental protein 5.";  
RL Biochem. Biophys. Res. Commun. 150:483-490(1988).  
RN ERRTUM.  
RA Buerzow R., Huhtala M.-L., Bohn H., Virtanen I., Seppaelae M.;  
RL Biochem. Biophys. Res. Commun. 151:630-631(1988).  
CC -1- FUNCTION: Seems to inhibit trypsin, factor VIIa/tissue factor,  
CC weakly factor Xa. Has no effect on thrombin.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Umbilical vein endothelial cells, liver,  
CC placenta, heart, pancreas, and maternal serum at advanced  
CC pregnancy.  
CC -1- DOMAIN: This inhibitor contains three inhibitory domains.  
CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL; D29992; BAA06272.1; -; mRNA.  
CC EMBL; L27624; AAA20094.1; -; mRNA.  
CC EMBL; AC002076; AAS02022.1; -; Genomic DNA.  
CC EMBL; AF217542; AK13254.1; -; Genomic DNA.  
CC EMBL; BC005330; AA05330.1; -; mRNA.  
CC PIR; A54951; A54951.  
CC HSSP; P10646; 11RH.  
CC DR Ensembl; ENSG0000105625; Homo sapiens.  
CC DR HGNC; HGNC:11761; TPPI2.  
CC H-InvDB; HIX000649; -.  
CC MIM; 600033; -.  
CC DR GO; GO:0005578; Extracellular matrix (sensu Metazoa); TAS.  
CC DR GO; GO:0005201; Extracellular matrix structural constituent, TAS.  
CC DR InterPro; IPR002223; Prot\_inh\_Kunz-m.  
CC DR InterPro; IPR008296; Prot\_inh\_TPPI.  
CC DR Pfam; PF00014; Kunitz\_BPTI; 3.  
CC DR PIRSF; PIRSF001620; TPPI\_1.  
CC DR PRINTS; PR00759; BASICPTASE.  
CC DR PRODOM; PD000222; Prot\_inh\_Kunz-m; 3.  
CC DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 2.  
CC DR PROSITE; PS0279; BPTI\_KUNITZ\_2; 3.  
CC DR Blood coagulation; Direct protein sequencing; Glycoprotein;  
CC KM Polymorphism; Protease inhibitor; Repeat; Serine protease inhibitor;  
CC KW Signal.  
CC FT SIGNAL. 1 22  
CC FT CHAIN 23 235 Tissue factor pathway inhibitor 2.  
CC FT DOMAIN 36 86 BPTI/Kunitz inhibitor 1.  
CC FT DOMAIN 96 149 BPTI/Kunitz inhibitor 2.  
CC FT DOMAIN 158 208 BPTI/Kunitz inhibitor 3.  
CC FT COMBINS 213 217 Poly-Lys.  
CC FT SITE 46 47 Reactive bond (By similarity).  
CC FT SITE 107 108 Reactive bond (By similarity).  
CC FT SITE 168 169 Reactive bond (By similarity).  
CC SITE 168 169

FT CARBOHYD 116 116 N-linked (GlcNAc...) (Potential).  
FT FT CARBOHYD 116 116 N-linked (GlcNAc...) (Potential).  
FT FT DISULFID 170 170 By similarity.  
FT FT DISULFID 36 86 By similarity.  
FT FT DISULFID 45 69 By similarity.  
FT FT DISULFID 61 82 By similarity.  
FT FT DISULFID 96 149 By similarity.  
FT FT DISULFID 106 130 By similarity.  
FT FT DISULFID 122 145 By similarity.  
FT FT DISULFID 158 208 By similarity.  
FT FT DISULFID 167 191 By similarity.  
FT FT DISULFID 183 204 By similarity.  
FT FT VARIANT 102 102 V->A (in dbSNP:1804202).  
FT FT CONFLICT 23 23 /FTID=VAR\_012005.  
FT FT SEQUENCE 235 AA; 26934 MW; 975ABA5C53F7C65F CRC64;  
SQ  
Query Match 100.0%; Score 1306; DB 1; Length 235;  
Best Local Similarity 100.0%; Pred. No. 5.4e-111;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDPAPPLGSLILLFLTEALGDAAQEPYNNALICLLPLDYGPCRALILRYRDRYTS 60  
DB 1 MDPAPPLGSLILLFLTEALGDAAQEPYNNALICLLPLDYGPCRALILRYRDRYTS 60  
QY 61 CRQPLYGCGEANNFTYWEACDCAWRLEKYPKVCRLQVSYDDQCEGSTEKYPFLSSM 120  
DB 61 CRQPLYGCGEANNFTYWEACDCAWRLEKYPKVCRLQVSYDDQCEGSTEKYPFLSSM 120  
QY 121 TCEKFFSGGCHNRLENNRPDPAATCGPCAPKRTSPCSPDEGLCSANNRYRNPY 180  
DB 121 TCEKFFSGGCHNRLENNRPDPAATCGPCAPKRTSPCSPDEGLCSANNRYRNPY 180  
QY 181 RTCDAPFTYTGCGANNFVSRDCRACAKALKKKKKPKLPAFRIRRIKKQF 235  
DB 181 RTCDAPFTYTGCGANNFVSRDCRACAKALKKKKKPKLPAFRIRRIKKQF 235  
DB 181 RTCDAPFTYTGCGANNFVSRDCRACAKALKKKKKPKLPAFRIRRIKKQF 235  
RESULT 2  
Q66M88 HUMAN PRELIMINARY; PRT; 235 AA.  
ID Q66M88;  
AC 066M88;  
DT 25-OCT-2004 (TRENBERL 28, Created)  
DT 25-OCT-2004 (TRENBERL 28, Last sequence update)  
DE Tissue factor pathway inhibitor 2.  
GN Name=TPPI2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
OC Homo.  
OC NCBI\_TaxID=9606;  
RN NUCLEOTIDE SEQUENCE.  
RP Xu Y., Li T., Du G.;  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.  
CC EMBL; AY691946; AAU04568.1; -; mRNA.  
CC DR GO; GO:0005576; Extracellular matrix.  
CC DR GO; GO:0030414; Protease inhibitor activity; IEA.  
CC DR GO; GO:0004867; Fibrinogen-type endopeptidase inhibitor activity; IEA.  
CC DR GO; GO:0007596; Fibrinogen-type endopeptidase inhibitor activity; IEA.  
CC DR GO; GO:0007596; Fibrinogen-type endopeptidase inhibitor activity; IEA.  
SQ SEQUENCE 235 AA; 26934 MW; 975ABA5C53F7C65F CRC64;  
Query Match 100.0%; Score 1306; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 5.4e-111;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDPAPPLGSLILLFLTEALGDAAQEPYNNALICLLPLDYGPCRALILRYRDRYTS 60  
DB 1 MDPAPPLGSLILLFLTEALGDAAQEPYNNALICLLPLDYGPCRALILRYRDRYTS 60  
QY 1 MDPAPPLGSLILLFLTEALGDAAQEPYNNALICLLPLDYGPCRALILRYRDRYTS 60  
DB 1 MDPAPPLGSLILLFLTEALGDAAQEPYNNALICLLPLDYGPCRALILRYRDRYTS 60  
QY 61 CRQPLYGCGEANNFTYWEACDCAWRLEKYPKVCRLQVSYDDQCEGSTEKYPFLSSM 120  
DB 61 CRQPLYGCGEANNFTYWEACDCAWRLEKYPKVCRLQVSYDDQCEGSTEKYPFLSSM 120

DB 61 CROFLVGGCGGNANFYTWACDCAWRIKVPKVCRLQVSVDDQCGSGSTKTFNNLSSM 120  
 QY 121 TCCKPFGGCHRRRIENRFPDEATCMGFCAPKIPSPCYSPKDBGLCSANVTYYFNPRY 180  
 DB 121 TCCKPFGGCHRRRIENRFPDEATCMGFCAPKIPSPCYSPKDBGLCSANVTYYFNPRY 180  
 QY 181 RTCDAPFTYTCGGGNDNNFVSRBDCRCACAKALKKKKMPLRFPASRIIRKIRKQF 235  
 DB 181 RTCDAPFTYTCGGGNDNNFVSRBDCRCACAKALKKKKMPLRFPASRIIRKIRKQF 235

RESULT 3  
 Q8NAK6\_HUMAN  
 ID Q8NAK6\_HUMAN PRELIMINARY; PRT; 224 AA.  
 AC Q8NAK6;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein FLJ35180.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 NCBI\_TaxID=9606;  
 [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Placenta;  
 PubMed=14702039; DOI=10.1038/ng1285;  
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,  
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,  
 RA Sekine M., Ohyashiki M., Nishi T., Shibahara T., Tanaka T., Ishii S.,  
 RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,  
 RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,  
 RA Shiratori A., Sudo H., Hosioki T., Kaku Y., Kodaira H., Komodo H.,  
 RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,  
 RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa K.,  
 RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,  
 RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y.,  
 RA Ishida S., Oho Y., Takiguchi S., Watanabe S., Yoshida M., Hotsuta T.,  
 RA Kusano Y., Kanehori K., Takahashi-Fujii A., Hara R., Tanase T.-O.,  
 RA Nomura Y., Togaiya S., Komai F., Hara R., Takeuchi K., Arita M.,  
 RA Inose N., Masehino K., Yuuki H., Ohlma A., Saeki K., Aota S.,  
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,  
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,  
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kakikami B.,  
 RA Hishigaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,  
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujisawa T.,  
 RA Oono T., Yamada K., Fujii Y., Ozaki K., Hiroo M., Ohmori Y.,  
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
 RA Ohtsuki R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
 RA Watanabe K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
 RA Togeashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Maeno Y., Yamashita R.,  
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isegai T., Sugano S.,  
 RT Complete sequencing and characterization of 21,443 full-length human  
 RT cDNAs.";  
 RL Nat. Genet. 36:40-45(2004).  
 CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.  
 DB EMBL; AK092499; BAC03906.1; -; mRNA.  
 DB HSSP; P10646; 1IRH.  
 DR GO; GO:0005576; C:extracellular region; IEA.  
 DR GO; GO:0030414; F:Protease inhibitor activity; IEA.  
 DR GO; GO:0004667; F:serine-type endopeptidase inhibitor activity; IEA.  
 DR GO; GO:0007596; F:blood coagulation; IEA.  
 DR InterPro; IPR002223; Prot\_inh\_Kunz-m.  
 DR InterPro; IPR008296; Prot\_inh\_Tppl.  
 DR Pfam; PF00014; Kunitz\_BPTI; 3.  
 DR PIRSF; PIRSF001620; TPPI; 1.  
 DR PRINTS; PR00759; BASICPTASB.  
 DR ProDom; PD000223; Prot\_inh\_Kunz-m; 3.  
 DR SMART; SM00131; KU; 3.

DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 2.  
 DR PROSITE; PS50279; BPTI\_KUNITZ\_2; 3.  
 SQ SEQUENCE 224 AA; 25795 MW; F586328C31344765 CRC64;  
 Query Match 94.3%; Score 1231.5; DB 2; Length 224;  
 Best Local Similarity 95.3%; Pred. No. 3.3e-104;  
 Matches 224; Conservative 0; Mismatches 0; Indels 11; Gaps 1;  
 QY 1 MDPARPLGLSILLFLTEALGDAQEPFGNNAEICLLPDVPCGALLIRYYDRYTOS 60  
 DB 1 MDPARPLGLSILLFLTEALGDAQEPF-----DYGPCALLIRYYDRYTOS 49  
 QY 61 CROFLVGGCGGNANFYTWACDCAWRIKVPKVCRLQVSVDDQCGSGSTKTFNNLSSM 120  
 DB 50 CROFLVGGCGGNANFYTWACDCAWRIKVPKVCRLQVSVDDQCGSGSTKTFNNLSSM 109  
 QY 121 TCCKPFGGCHRRRIENRFPDEATCMGFCAPKIPSPCYSPKDBGLCSANVTYYFNPRY 180  
 DB 110 TCCKPFGGCHRRRIENRFPDEATCMGFCAPKIPSPCYSPKDBGLCSANVTYYFNPRY 169  
 QY 181 RTCDAPFTYTCGGGNDNNFVSRBDCRCACAKALKKKKMPLRFPASRIIRKIRKQF 235  
 DB 170 RTCDAPFTYTCGGGNDNNFVSRBDCRCACAKALKKKKMPLRFPASRIIRKIRKQF 224

RESULT 4  
 Q8NE89\_HUMAN  
 ID Q8NE89\_HUMAN PRELIMINARY; PRT; 167 AA.  
 AC Q8NE89;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Similar to tissue factor pathway inhibitor 2 (Fragment).  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 NCBI\_TaxID=9606;  
 [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Placenta;  
 RA Strauberg R.;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.  
 DB EMBL; BC034155; AA034155.1; -; mRNA.  
 DR HSSP; P10646; 1IRH.  
 DR GO; GO:0004667; F:serine-type endopeptidase inhibitor activity; IEA.  
 DR InterPro; IPR002223; Prot\_inh\_Kunz-m.  
 DR Pfam; PF00014; Kunitz\_BPTI; 3.  
 DR PRINTS; PR00759; BASICPTASB.  
 DR ProDom; PD000223; Prot\_inh\_Kunz-m; 3.  
 DR SMART; SM00131; KU; 2.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
 DR PROSITE; PS50279; BPTI\_KUNITZ\_2; 2.  
 FT NON TER 1  
 SQ SEQUENCE 167 AA; 19365 MW; 16C204B96071F27D CRC64;  
 Query Match 72.2%; Score 943; DB 2; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-78;  
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 69 CEGNANFYTWACDCAWRIKVPKVCRLQVSVDDQCGSGSTKTFNNLSSMCEKFPFG 128  
 DB 1 CEGNANFYTWACDCAWRIKVPKVCRLQVSVDDQCGSGSTKTFNNLSSMCEKFPFG 60  
 QY 129 GCHRRRIENRFPDEATCMGFCAPKIPSPCYSPKDBGLCSANVTYYFNPRYRTCAFTY 188  
 DB 61 GCHRRRIENRFPDEATCMGFCAPKIPSPCYSPKDBGLCSANVTYYFNPRYRTCAFTY 120  
 QY 189 TGGGNDNNFVSRBDCRCACAKALKKKKMPLRFPASRIIRKIRKQF 235  
 DB 121 TGGGNDNNFVSRBDCRCACAKALKKKKMPLRFPASRIIRKIRKQF 167



```

RESULT 5
Q7YR08 BOVIN
ID Q7YR08 BOVIN PRELIMINARY; PRT; 234 AA.
AC Q7YR08
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE Tissue factor pathway inhibitor-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22802738; PubMed=12921785; DOI=10.1016/S0003-9661(03)00332-1;
RA Du X., Deng P.M., Chand H.S., Kistiel W.,
RT "Molecular cloning, expression, and characterization of bovine tissue
factor pathway inhibitor-2."
RL Arch. Biochem. Biophys. 417:96-104(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Deng P.-M., Kistiel W., Sun T.-T.,
RT Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
DR EMBL; AY234861; A0804035.1; -, mRNA.
DR HSSP; P00981; 1DTK.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0030414; F:protease inhibitor activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008296; Prot_inh_TFPI.
DR Pfam; PF00014; Kunitz_BPTI; 3.
DR PIRSF; PIRSF01620; TFPI; 1.
DR PRINTS; PR00759; BASICTPASE.
DR PRODOM; PD000222; Prot_inh_Kunz-m; 3.
DR SMART; SM00131; KU; 3.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 3.
SQ SEQUENCE 234 AA; 26675 MW; 401EBC84D589B422 CRC64;

Query Match 71.9%; Score 939.5; DB 2; Length 234;
Best Local Similarity 72.2%; Pred. No. 1.5e-77;
Matches 171; Conservative 23; Mismatches 38; Indels 5; Gaps 3;

QY 1 MDPARPLGSIILLFLTEALGDAAQEPGNNAEICLLPLDYGPCRALLRYYDRTOS 60
DB 1 MDSVRLPLMLLSLLLVGTLGASQAPPGNNAEICLLPPDDGPCRARIPSYDDRTOS 60
QY 61 CROFLYGGCEGNANFYTWACDCAWRIRKVPVCHLQVSVDDCGEGSTKFFNLISM 120
DB 61 CRFPWGGCEGNANFYTWACDCAWRIRKVPVCHLQVSVDDCGEGSTKFFNLISM 119
QY 121 TCSEKPSGGCHRRRIENRPDEATCMGFCAPKKI-IPSCYSPKDEGLCSANVTYYFNPR 180
DB 120 TCCKFTISGGCHSN--ENRPDEATCMDFCAPKRAPVGYCPKDEGLCSANVTYYFNPR 177
QY 181 RTGDAFTYGGCGGNDNNFVRBEDCKACAKLKKK--KKPKRFPASRIKRIKKOP 235
DB 178 KACEAFNRYTGCGGNDNNFVNLKDCCKTCVAKLKKKKPKRLLANRLKIKKOP 234

RESULT 6
O8CF99 RAT
ID O8CF99 RAT PRELIMINARY; PRT; 230 AA.
AC O8CF99
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE Tissue factor pathway inhibitor-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22802738; PubMed=12921785; DOI=10.1016/S0003-9661(03)00332-1;
RA Du X., Deng P.M., Chand H.S., Kistiel W.,
RT "Molecular cloning, expression, and characterization of bovine tissue
factor pathway inhibitor-2."
RL Arch. Biochem. Biophys. 417:96-104(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Deng P.-M., Kistiel W., Sun T.-T.,
RT Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
DR EMBL; AY234861; A0804035.1; -, mRNA.
DR HSSP; P00981; 1DTK.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0030414; F:protease inhibitor activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008296; Prot_inh_TFPI.
DR Pfam; PF00014; Kunitz_BPTI; 3.
DR PIRSF; PIRSF01620; TFPI; 1.
DR PRINTS; PR00759; BASICTPASE.
DR PRODOM; PD000222; Prot_inh_Kunz-m; 3.
DR SMART; SM00131; KU; 3.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 3.
SQ SEQUENCE 230 AA; 26157 MW; 07CCD5B9F7D43BD9 CRC64;

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OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague Dawley; TISSUE=Placenta;
RX MEDLINE=22183372; PubMed=12195712;
RA Hiseaka T., Kistiel W., Rosenbaum J.,
RT "cDNA cloning and tissue distribution of the rat ortholog of tissue
factor pathway inhibitor-2."
RL Thromb. Haemost. 88:356-357(2002).
CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
DR EMBL; AJ428954; CAD22046.1; -, mRNA.
DR HSSP; P10646; 1IRH.
DR Ensemble; ENSRNOC0000010513; Rattus norvegicus.
DR RCD; 628629; TFPI2.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0030414; F:protease inhibitor activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008296; Prot_inh_TFPI.
DR Pfam; PF00014; Kunitz_BPTI; 3.
DR PIRSF; PIRSF01620; TFPI; 1.
DR PRINTS; PR00759; BASICTPASE.
DR PRODOM; PD000222; Prot_inh_Kunz-m; 3.
DR SMART; SM00131; KU; 3.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 3.
KW Signal.
FT CHAIN 1 25 Potential.
FT 25 230 tissue factor pathway inhibitor-2.
SQ SEQUENCE 230 AA; 26157 MW; 07CCD5B9F7D43BD9 CRC64;

Query Match 50.1%; Score 654; DB 2; Length 230;
Best Local Similarity 55.6%; Pred. No. 1.7e-51;
Matches 129; Conservative 25; Mismatches 74; Indels 4; Gaps 3;

QY 1 MDPARPLGSIILLFLTEALGDAAQEPGNNAEICLLPLDYGPCRALLRYYDRTOS 60
DB 1 MDPATSLRLMNPPLLVGSLGASVSAQGNNAEICLLPLDYGPCRALLRYYDRTOS 60
QY 61 CROFLYGGCEGNANFYTWACDCAWRIRKVPVCHLQVSVDDCGEGSTKFFNLISM 120
DB 61 CRFPKYGCGGNANFYTWACDCAWRIRKVPVCHLQVSVDDCGEGSTKFFNLISM 119
QY 121 TCSEKPSGGCHRRRIENRPDEATCMGFCAPKKI-IPSCYSPKDEGLCSANVTYYFNPR 179
DB 120 TCSEPLRPLGLC--SRITNVPEPEAMCKSLCEPRKSIIPSCSPKDEGLCSANVTYYFNPR 177
QY 180 YRTCDAPFTYTGCGGNDNNFVRBEDCKRACAKLKKKKPKRFPASRIKRIK 231
DB 178 NRTCEFTYTGCGGNDNNFYLDACNRCACVAKLKKRKRRIKIDGFLRPMWLR 229

RESULT 7
TFPI2 MOUSE
ID TFPI2 MOUSE STANDARD; PRT; 230 AA.
AC Q35356
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Tissue factor pathway inhibitor 2 precursor (TFPI-2).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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CC STRAIN-1CR: TISSUE=Placenta;  
 RX MEDLINE=97101108; PubMed=8945635;  
 RA Miyagi Y., Yasumitsu H., Mizushima H., Koshikawa N., Matsuda Y.,  
 RA Itoh Y., Hori T., Aoki I., Mitsuoka K., Miyazaki K.;  
 RT "Cloning of the cDNA encoding mouse pps/TPPI-2 and mapping of the gene  
 to chromosome 6.";  
 RL Cell Biol. 15:947-954(1996).  
 RN  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=129/5VJ;  
 RX MEDLINE=20132652; PubMed=10669168;  
 RA Kazana Y., Kamel S., Kuyper J.L., Foster D.C., Kistiel W.;  
 RT "Nucleotide sequence of the gene encoding murine tissue factor pathway  
 inhibitor-2.";  
 RL Thromb. Haemost. 83:141-147(2000).  
 RN  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC STRAIN=C57BL/6J; TISSUE=Mammary gland;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
 RA Klausner R.D., Collins P.S., Wagner L., Sherman C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Tothlyuk S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huijyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,  
 RA Pabey J., Helton E., Kettman M., Madan A.C., Shevchenko Y., Bouffard G.G.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: Seems to inhibit trypsin, factor VIIa/tissue factor,  
 -1- weakly factor Xa. Has no effect on thrombin.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Highly expressed in placenta. Also expressed  
 in liver and kidney.  
 CC -1- DOMAIN: This inhibitor contains three inhibitory domains.  
 CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.  
 CC  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.  
 CC  
 CC EMBL: D50586; BAA22585.1; -; mRNA.  
 DR EMBL: AP180353; AAP40412.1; -; Genomic DNA.  
 DR EMBL: BC021639; AAP21639.1; -; mRNA.  
 DR HSSP: P10646; IIRH.  
 DR Ensembl: ENSMUSG00000029664; Mus musculus.  
 DR MGI: MGI:108543; Tfp12.  
 DR GO: GO:0005615; C:extracellular space; TAS.  
 DR InterPro: IPR002223; Prot\_inh\_Kunz-m.  
 DR InterPro: IPR008296; Prot\_inh\_TFPI.  
 DR Pfam: PF00014; Kunitz\_BPTI; 3.  
 DR PIRSF: PIRSF001620; TFPI; 1.  
 DR PRINTS: PR00759; BASICTPASE.  
 DR PRODOM: PD000222; Prot\_inh\_Kunz-m; 3.  
 DR SMART: SMO0131; KU; 3.  
 DR PROSITE: PS00280; BPTI\_KUNITZ\_1; 2.  
 DR PROSITE: PS00279; BPTI\_KUNITZ\_2; 3.  
 KW Blood coagulation, glycoprotein, Protease inhibitor, Repeat,  
 KW Serine protease inhibitor, Signal.  
 FT SIGNAL 1 22 By similarity.  
 FT CHAIN 23 230 Tissue factor pathway inhibitor 2.

FT DOMAIN 36 86 BPTI/Kunitz inhibitor 1.  
 FT DOMAIN 96 146 BPTI/Kunitz inhibitor 2.  
 FT DOMAIN 156 205 BPTI/Kunitz inhibitor 3.  
 FT SITE 46 47 Reactive bond (by similarity).  
 FT SITE 106 107 Reactive bond (by similarity).  
 FT SITE 166 167 Reactive bond (by similarity).  
 FT CARBOHYD 168 168 N-linked (GlcNAc...) (potential).  
 FT CARBOHYD 178 178 N-linked (GlcNAc...) (potential).  
 FT DISULFID 36 86 By similarity.  
 FT DISULFID 45 69 By similarity.  
 FT DISULFID 61 82 By similarity.  
 FT DISULFID 96 146 By similarity.  
 FT DISULFID 105 129 By similarity.  
 FT DISULFID 121 142 By similarity.  
 FT DISULFID 156 205 By similarity.  
 FT DISULFID 165 189 By similarity.  
 FT DISULFID 181 202 By similarity.  
 SQ DISULFID 230 AA; 26137 MW; 57EADB2E36521C7B CRC64;  
 Query Match 49.3%; Score 644; DB 1; Length 230;  
 Best Local Similarity 56.4%; Pred. No. 1, 4e-50;  
 Matches 123; Conservative 26; Mismatches 65; Indels 4; Gaps 3;  
 QY 1 MDPARPLGSLILFLTEALGDAQEPGNNABICLLPVDYPCRALIRYIDRYTQS 60  
 DB 1 MDPAMPPLQMLNPLLVGLVGLTSAQGNNEICLLPADAGPCMLIPKPYDRDQOK 60  
 QY 61 CRQFLVGGCGGANNPTTWEACDCAKRIKVRKVRQLQVSDQCGESTKXKFNLSM 120  
 DB 61 CRFPVGGCGGANNPTTWEACDCAKRIKVRKVRQLQVSDQCGESTKXKFNLSM 119  
 QY 121 TCERFSGGCHRRIRIENRPPDCAKMGFCAPK-IPSCFSPKDEGLCSANVTREYENPR 179  
 DB 120 TCERFLRGGLC-SRTIVFSEAKTKGLCEPRKHIPFCSPDDEGLCSANVTREYENPR 177  
 QY 180 YRTCDATYTCGCGNDNFVSRBDCKRCAKALKKKK 217  
 DB 178 NKCEFTTYGCGGNNFFYLDACGRACVGMKKPKR 215  
 RESULT 8  
 ID 077025 XENLA PRELIMINARY; PRT; 224 AA.  
 AC 077025;  
 DT 01-OCT-2003 (TREMblrel. 25, Created)  
 DT 01-OCT-2003 (TREMblrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TREMblrel. 25, Last annotation update)  
 DE MGC68843 protein.  
 OS Xenopus laevis (African clawed frog).  
 CC Bakaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 CC Xenopodinae; Xenopus; Xenopus.  
 CC NCBI\_TaxID=8355;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryo;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
 RA Klausner R.D., Collins P.S., Wagner L., Sherman C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Tothlyuk S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huijyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,  
 RA Pabey J., Helton E., Kettman M., Madan A.C., Shevchenko Y., Bouffard G.G.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryo;  
 RA MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RA Richardson P., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 RT Initiative.";  
 RL Dev. Dyn. 225:384-391(2002).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryo;  
 RA Klein S., Strausberg R.;  
 RA Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.  
 DR EMBL; BC055972; AAH55972.1; -, mRNA.  
 DR HSBP; P00974; 1BP1.  
 DR GO; GO:0005576; C:extracellular region; IEA.  
 DR GO; GO:0030414; F:protease inhibitor activity; IEA.  
 DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.  
 DR GO; GO:0007596; P:blood coagulation; IEA.  
 DR InterPro; IPR002223; ProtInh\_Kunz-m.  
 DR Pfam; PF00014; Kunitz\_BPTI; 3.  
 DR PIRSF; PIRSF001620; TFP1; 1.  
 DR PRINTS; PR00759; BASICPTASE.  
 DR ProDom; PD000222; ProtInh\_Kunz-m; 3.  
 DR SMART; SM00131; KU; 3.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 3.  
 DR PROSITE; PS0279; BPTI\_KUNITZ\_2; 3.  
 SQ SEQUENCE 224 AA; 25538 MW; 11C2D1C4C789445B CRC64;  
 Query Match 48.6%; Score 635; DB 2; Length 224;  
 Best Local Similarity 53.5%; Pred. No. 9e-50;  
 Matches 107; Conservative 35; Mismatches 50; Indels 8; Gaps 4;  
 QY 28 PGNNAEICLLPDDYGPCRALILRIYYDRYQSCROFLYGGCGGNANFYTWACDADCM 87  
 DB 22 PMQGNITVCLLPDDGPCKALIPHYYYDRYQTCGFPGGCGGNANFYTWACDADCM 81  
 QY 88 RIEKVPKCRLOVSVDDCGESTKCYFNLSSMTCEKFFSGGCHNRRIENRPDEATCKG 147  
 DB 82 KIKKVPKACRM-VPDGCPGRGTYKRYAYNMKTRCQFLYGGCYGN--DNNPDQDSCIN 138  
 QY 148 FCAPKK-IPSPCYSPKDEGLCSANVTIRYFNPRTCDAFYTYGGCGDNFNFSREDCKR 206  
 DB 139 FCAPRDAPSPCYSPKDEGSCASVTRIRYFNIESKACEFVYTYGGCGSNFNFKYEDCD 198  
 QY 207 ACAKALKKKK---KMPKLR 222  
 DB 199 VCKKGTGRPRNQPKIRIR 218  
 RESULT 9  
 OSFYV6\_XENTR PRELIMINARY; PRT; 219 AA.  
 ID OSFYV6\_XENTR PRELIMINARY; PRT; 219 AA.  
 AC OSFYV6;  
 DT 10-MAY-2005 (Tremblrel. 30, Created)  
 DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)  
 DE MGCL08301 protein.  
 GN Name=MGCL08301;  
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Batelaeostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus; Silurana.  
 CX NCBI\_Taxid=8364;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Whole body;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Diachenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McGwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Small D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Whole body;  
 RA Klein S., Gerhard D.S.;  
 RA Submitted (Feb-2005) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.  
 DR EMBL; BC089705; AAH9705.1; -, mRNA.  
 DR GO; GO:0005576; C:extracellular region; IEA.  
 DR GO; GO:0030414; F:protease inhibitor activity; IEA.  
 DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.  
 DR GO; GO:0007596; P:blood coagulation; IEA.  
 DR InterPro; IPR002223; ProtInh\_Kunz-m.  
 DR Pfam; PF00014; Kunitz\_BPTI; 3.  
 DR PIRSF; PIRSF001620; TFP1; 1.  
 DR PRINTS; PR00759; BASICPTASE.  
 DR ProDom; PD000222; ProtInh\_Kunz-m; 3.  
 DR SMART; SM00131; KU; 3.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 3.  
 DR PROSITE; PS0279; BPTI\_KUNITZ\_2; 3.  
 SQ SEQUENCE 219 AA; 29449 MW; 8PF6AD89B8556C8 CRC64;  
 Query Match 48.2%; Score 630; DB 2; Length 219;  
 Best Local Similarity 52.7%; Pred. No. 2.5e-49;  
 Matches 108; Conservative 35; Mismatches 54; Indels 8; Gaps 4;  
 QY 28 PGNNAEICLLPDDYGPCRALILRIYYDRYQSCROFLYGGCGGNANFYTWACDADCM 87  
 DB 21 PMQGNITVCLLPDDGPCKALIPHYYYDRYQTCGFPGGCGDNFNFKYEDCD 80  
 QY 88 RIEKVPKCRLOVSVDDCGESTKCYFNLSSMTCEKFFSGGCHNRRIENRPDEATCKG 147  
 DB 81 KIKKVPKACRM-DGCPGRGTYKRYAYNMKTRCQFLYGGCYGN--DNNPDQDSCIN 137  
 QY 148 FCAPKK-IPSPCYSPKDEGLCSANVTIRYFNPRTCDAFYTYGGCGDNFNFSREDCKR 206  
 DB 138 FCAPRDAPSPCYSPKDEGSCASVTRIRYFNIESKACEFVYTYGGCGSNFNFKYEDCD 197  
 QY 207 ACAKALKKKKMPKLRIRIR 231  
 DB 198 VC---KKGSRPRNRIRIRIR 218  
 RESULT 10  
 QARDL7\_TETNG PRELIMINARY; PRT; 190 AA.  
 ID QARDL7\_TETNG PRELIMINARY; PRT; 190 AA.  
 AC QARDL7;  
 DT 13-SEP-2005 (Tremblrel. 31, Created)  
 DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)  
 DE 13-SEP-2005 (Tremblrel. 31, Last annotation update)  
 DE Chromosome undetermined SCAF16203, whole genome shotgun sequence.

GN ORFNames=GSTENG00038126001;  
 OS Tetradon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetradontiformes;  
 OC Tetradontidae; Tetradontidae; Tetradon.  
 NCBI\_TaxID=99883;  
 [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
 Maucell B., Bouneau L., Fischer C., Ozouf-Coetzee C., Bernot A.,  
 Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
 Desliva C., Sattoum M., Levy M., Boudet N., Castellano S.,  
 Anthouard V., Jubin C., Castellani V., Kallika M., Vacherie B.,  
 Clement C., Skalli Z., Cattolico L., Poulain J., De Bernardis V.,  
 Cruaud C., Duprat S., Broctier P., Coutanceau J.P., Gouzy J.,  
 Parra G., Lardier G., Chapelle C., McKernan K.J., McMan P., Bosak S.,  
 Kellis M., Volff J.N., Gulgo R., Zody M.C., Mesirov J.,  
 Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 Laudat V., Schacherer V., Quetier F., Saurin W., Scarpelli C.,  
 Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.,  
 RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.,  
 RT "the early vertebrate proto-karyotype".  
 RL Nature 431:946-957(2004).  
 RN [2]  
 CC NUCLEOTIDE SEQUENCE.  
 RP Genoscope, Whitehead Institute Centre for Genome Research;  
 RG Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 CC -1- SIMILARITY: Contains 3 BPT1/Kunitz inhibitor domains.  
 DR EMBL: CA801016203; CAG13515.1; -, Genomic DNA.  
 DR InterPro: IPR002223; Prot\_inh\_Kunz-m.  
 DR Pfam: PF00014; Kunitz BPT1; 3.  
 DR PRINTS: PR00759; BASICPTASE.  
 DR Prodom: PD000222; Prot\_inh\_Kunz-m; 3.  
 DR SMART: SM00131; KU\_3.  
 DR PROSITE: PS00280; BPT1\_KUNITZ\_1; 2.  
 DR PROSITE: PS50279; BPT1\_KUNITZ\_2; 3.  
 SQ SEQUENCE 190 AA; 21614 MW; 8A7EC6515605ECD CRC64;  
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 Best Local Similarity 47.6%; Pred. No. 1,1e-33; Indels 4; Gaps 3;  
 Matches 79; Conservative 28; Mismatches 55;  
 QY 35 ICLPLDYGPCRALILRYDYRYSQCRQFLYGGCEGNANFYTWACDDACWRIEKVPK 94  
 DB 26 VCLIQVNEGCRDRIHYNTITTKCELFYSYGGCGGNANFRSFGCQKTCRIRPIQ 85  
 QY 95 VCLIQVSVDDQCGSTERYFPNLSSMTCEKFPSCGCHRNRIENRFPDEATCMGFCAP 153  
 DB 86 ICRFPQGV-SPCRALILAKYFPNMTMQCEBFFYGGCLGS--SNRFDLASCKEYCSPHKS 142  
 QY 154 IPRFVSPKDEGLCSANVTYRFRRTGDAFTYTCGGDNDFV 199  
 DB 143 LPLVLCIDPLDKGCSAFPRYYNKATKCEBFIYSGGGANSKPV 188  
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 AC QSRP98;  
 DT 01-FEB-2005 (TREMBlrel. 29, Created)  
 DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)  
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)  
 DE Hypothetical protein DKFp469B1122.  
 GN Name=DKFp469B1122;  
 OS Pongo pygmaeus (Orangutan).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;  
 OC Pongo.  
 NCBI\_TaxID=9600;

RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC Tissue-Kidney.  
 RG The German cDNA Consortium;  
 RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Oanger A., Fodor G.,  
 Han M., Miemann S.;  
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Contains 3 BPT1/Kunitz inhibitor domains.  
 DR EMBL: CB857263; CAH89559.1; -, mRNA.  
 DR SMR: QSRP98; 121-178, 210-270.  
 DR GO: GO:0005576; Cytoplasmic region; IEA.  
 DR GO: GO:0030414; F-actinase inhibitor activity; IEA.  
 DR GO: GO:004847; F-actin-type endopeptidase inhibitor activity; IEA.  
 DR GO: GO:007596; Blood coagulation; IEA.  
 DR InterPro: IPR002223; Prot\_inh\_Kunz-m.  
 DR InterPro: IPR002296; Prot\_inh\_Kunz-m.  
 DR Pfam: PF00014; Kunitz BPT1; 3.  
 DR PIRSF: PIRSF001620; TFP1; 1.  
 DR PRINTS: PR00759; BASICPTASE.  
 DR Prodom: PD000222; Prot\_inh\_Kunz-m; 3.  
 DR SMART: SM00131; KU\_3.  
 DR PROSITE: PS00280; BPT1\_KUNITZ\_1; 3.  
 DR PROSITE: PS50279; BPT1\_KUNITZ\_2; 3.  
 KW Hypothetical protein.  
 SQ SEQUENCE 304 AA; 34861 MW; 6DF1A1DE3F61PC0 CRC64;  
 Query Match 30.3%; Score 396; DB 2; Length 304;  
 Best Local Similarity 30.6%; Pred. No. 8e-28; Indels 76; Gaps 8;  
 Matches 87; Conservative 37; Mismatches 84;  
 QY 12 LILFLTEALGDAQBPRTGNA-----EICLLPLDYGPCRALILRYDYRYS 58  
 DB 17 LILNLAPALPLNDSEDBGHTITTDLPPLKMHSPFCFKADBDGCKALMKRFPFNIF 76  
 QY 59 QSCRQFLYGGCEGNANFYTWACDDACWR-----IEKVPKCVLQVSVDDQ-- 105  
 DB 77 RQCEBFIYGGCEGNQRFPSLEBQCKMCTRDVANKIKITTLQOEKEDFCELE--BDP 133  
 QY 106 CEESTERYFPNLSSMTCEKFPSCGCHRNRIENRFPDEATCMGFC----- 149  
 DB 134 CRGYITRYNNQTKQCEBFIYGGCLGNM--NNFETLEBCKNTCBGPNQFQVNDYGTOL 191  
 QY 150 -----APKCI-----PSFCYSPDEGLCSANVTYRFRRTGDAFTYTCG 192  
 DB 192 MAGNMLTQSTVYSLFPHGHSWCLTPADRLCSANRFRFYNSVIGKCRFPKSGCG 251  
 QY 193 GNDNPFVSRBDCRACAKAL-----KCKKMPKLRPA 224  
 DB 252 GNNNTFTSKOECIRACKKGFIRISKGLIKTKRKRRKQKVIA 295  
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 AC P10646; O95103;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Tissue factor pathway inhibitor precursor (TFPI) (lipoprotein-  
 DE associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)  
 DE (BPI).  
 GN Name=TFPI; Synonyms=LACI, TFP11;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;  
 OC Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE (ISOFORM ALPHA).  
 RX MEDLINE=8818127; PubMed=2452157;  
 RA Wu T.-C., Kremer K.K., Girard T.J., Miletich J.P., Broze G.J. Jr.;  
 RT "Cloning and characterization of a cDNA coding for the lipoprotein-  
 associated coagulation inhibitor shows that it consists of three

RT tandem Kunitz-type inhibitory domain.";  
RL J. Biol. Chem. 263:6001-6004(1988).  
RN [2]  
RP NUCLEOTIDE SEQUENCE (ISOFORM ALPHA).  
RX MEDLINE=9112927; PubMed=1993173;  
RA van der Logt C.P.B., Reitema P.H., Bertina R.M.;  
RT "Intron-exon organization of the human gene coding for the  
RT lipoprotein-associated coagulation inhibitor: the factor Xa dependent  
RT inhibitor of the extrinsic pathway of coagulation.";  
RL Biochemistry 30:1571-1577(1991).  
RN [3]  
RP NUCLEOTIDE SEQUENCE (ISOFORM ALPHA).  
RX MEDLINE=91161593; PubMed=2002045;  
RA Girard T.J., Eddy R., Wesselschmidt R.L., Macphail L.A., Likert K.M.,  
RA Byers M.G., Shows T.B., Broze G.J. Jr.;  
RT "Structure of the human lipoprotein-associated coagulation inhibitor  
RT gene. Intron/exon gene organization and localization of the gene to  
RT chromosome 2.";  
RL J. Biol. Chem. 266:5036-5041(1991).  
RN [4]  
RP NUCLEOTIDE SEQUENCE (ISOFORM ALPHA).  
RX MEDLINE=99388722; PubMed=2781520; DOI=10.1016/0049-3848(89)90454-4;  
RA Girard T.J., Warren L.A., Novotny W.F., Bejcek B.E., Miletich J.P.,  
RA Broze G.J. Jr.;  
RT "Identification of the 1.4 kb and 4.0 kb messages for the lipoprotein  
RT associated coagulation inhibitor and expression of the encoded  
RT protein.";  
RL Thromb. Res. 55:37-50(1989).  
RN [5]  
RP NUCLEOTIDE SEQUENCE (ISOFORM BETA).  
RX Chang J.-Y., Monroe D.M., Roberts H.R.;  
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).  
RA Rieder M.J., Carrington D.P., da Ponte S.H., Haecings N.C.,  
RA Ahearn M.O., Kildanek S.A., Rajkumar N., Toth E.J., Yi Q.,  
RA Nickerson D.A.;  
RT "SeacatSNP: NHLBI HL6682 program for genomic applications, UW-  
RT FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM BETA).  
RC T1850E=Pancreas;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altshuler S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshynski S., Carninci P., Prange C.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Millar S.J.,  
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,  
RA Villalón D.K., Muny D.M., Sodergren B.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues Y., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Sherchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [8]  
RP PROTEIN SEQUENCE OF 29-50.  
RX MEDLINE=90036996; PubMed=2553722;  
RA Novotny W.F., Girard T.J., Miletich J.P., Broze G.J. Jr.;  
RT "Purification and characterization of the lipoprotein-associated  
RT coagulation inhibitor from human plasma.";  
RL J. Biol. Chem. 264:18832-18837(1989).  
RN [9]  
RP PROTEIN SEQUENCE OF 29-43.  
RX PubMed=15340161; DOI=10.1110/ps.04682504;  
RA Zhang Z., Henzel W.J.;  
RT "Signal peptide prediction based on analysis of experimentally  
RT verified cleavage sites.";  
RL Protein Sci. 13:2819-2824(2004).  
RN [10]  
RP INHIBITORY SITES.  
RX MEDLINE=89181950; PubMed=2927510; DOI=10.1038/336518a0;  
RA Girard T.J., Warren L.A., Novotny W.F., Likert K.M., Brown S.G.,  
RA Miletich J.P., Broze G.J. Jr.;  
RT "Functional significance of the Kunitz-type inhibitory domains of  
RT lipoprotein-associated coagulation inhibitor.";  
RL Nature 338:518-520(1989).  
RN [11]  
RP CARBOHYDRATE-LINKAGE SITES.  
RX MEDLINE=96224851; PubMed=8639592; DOI=10.1021/bi9524880;  
RA Nakahara Y., Miyata T., Hamuro T., Funatsu A., Miyagi M.,  
RA Tanasawa S., Kato H.;  
RT "Amino acid sequence and carbohydrate structure of a recombinant human  
RT tissue factor pathway inhibitor expressed in Chinese hamster ovary  
RT cells: one N- and two O-linked carbohydrate chains are located between  
RT Kunitz domains 2 and 3 and one N-linked carbohydrate chain is in  
RT Kunitz domain 2.";  
RL Biochemistry 35:6450-6459(1996).  
RN [12]  
RP REVIEW.  
RX MEDLINE=91104709; PubMed=2271516;  
RA Broze G.J. Jr., Girard T.J., Novotny W.F.;  
RT "Regulation of coagulation by a multivalent Kunitz-type inhibitor.";  
RL Biochemistry 29:7539-7546(1990).  
RN [13]  
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 121-178 IN COMPLEX WITH  
RP TRYPSIN.  
RX MEDLINE=97390427; PubMed=9242660; DOI=10.1074/jbc.272.32.19931;  
RA Stubbs M.T., Morenweiser R., Stuerzbecher J., Bauer M., Bode W.,  
RA Huber R., Plechotcka G.P., Matchner G., Sommerhoff C.P., Fritz H.,  
RA Auerwald R.A.;  
RT "The three-dimensional structure of recombinant leech-derived trypsin  
RT inhibitor in complex with trypsin. Implications for the structure of  
RT human mast cell trypsinase and its inhibition.";  
RL J. Biol. Chem. 272:19931-19937(1997).  
RN [14]  
RP STRUCTURE BY NMR OF 121-182.  
RX MEDLINE=97342711; PubMed=9199408; DOI=10.1006/jmbi.1997.1029;  
RA Burgering M.J.M., Orbons L.P.M., van der Doelen A., Milders J.,  
RA Theunissen H.J.M., Groocenhuis P.D.J., Bode W., Huber R., Stubbs M.T.;  
RT "The second Kunitz domain of human tissue factor pathway inhibitor:  
RT cloning, structure determination and interaction with factor Xa.";  
RL J. Mol. Biol. 269:395-407(1997).  
RN [15]  
RP STRUCTURE BY NMR OF 210-270.  
RX MEDLINE=21633982; PubMed=11772005; DOI=10.1021/bi011299g;  
RA Mine S., Yamazaki T., Miyata T., Hara S., Kato H.;  
RT "Structural mechanism for heparin-binding of the third Kunitz domain  
RT of human tissue factor pathway inhibitor.";  
RL Biochemistry 41:78-85(2002).  
RN [16]  
RP VARIANT MET-292.  
RX MEDLINE=99318093; PubMed=10391209; DOI=10.1038/10290;  
RA Carcilli M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,  
RA Shaw N., Lane C.R., Lim B.P., Kalyanaraman N., Nemes J., Zlaugta L.,  
RA Friedland L., Rolfe A., Warrington J., Lipschutz R., Daley G.O.,  
RA Lander E.S.;  
RT "Characterization of single-nucleotide polymorphisms in coding regions  
RT of human genes.";  
RL Nat. Genet. 22:231-238(1999).  
RN [17]  
RP ERRATUM.  
RA Carcilli M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,  
RA Shaw N., Lane C.R., Lim B.P., Kalyanaraman N., Nemes J., Zlaugta L.,  
RA Friedland L., Rolfe A., Warrington J., Lipschutz R., Daley G.O.,  
RA Lander E.S.;  
RT Nat. Genet. 23:373-373(1999).

```

CC -1- FUNCTION: Inhibits factor X (X(a)) directly and, in a Xa-dependent
CC way, inhibits VIIa/cis-enzyme factor activity, presumably by forming a
CC quaternary Xa/LaCII/VIIa/TF complex. It possesses an antithrombotic
CC action and also the ability to associate with lipoproteins in
CC plasma.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Alpha; Synonym=alpha1;
CC IsoId=PI0646-1; Sequence=displayed;
CC Name=Beta; Synonym=alpha2;
CC IsoId=PI0646-2; Sequence=VSP_003030, VSP_003031;
CC -1- TISSUE SPECIFICITY: Mostly in endothelial cells.
CC -1- DOMAIN: This inhibitor contains three inhibitory domains. The
CC first domain interacts with VIIa and TF, the second one with Xa.
CC -1- PTM: O-glycosylated.
CC -1- SIMILARITY: Contains 3 BPT/Kunitz inhibitor domains.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL, J03225; AAA52022.1; -; mRNA.
CC EMBL, M58650; AAA59480.1; -; Genomic_DNA.
CC EMBL, M58645; AAA59480.1; JOINED; Genomic_DNA.
CC EMBL, M58646; AAA59480.1; JOINED; Genomic_DNA.
CC EMBL, M58647; AAA59480.1; JOINED; Genomic_DNA.
CC EMBL, M58648; AAA59480.1; JOINED; Genomic_DNA.
CC EMBL, M58649; AAA59480.1; JOINED; Genomic_DNA.
CC EMBL, M59459; AAA59526.1; -; Genomic_DNA.
CC EMBL, M59493; AAA59526.1; JOINED; Genomic_DNA.

Query Match      29.7%; Score 388; DB 1; Length 304;
Best Local Similarity 30.3%; Pred. No. 4,3e-27;
Matches 86; Conservative 37; Mismatches 85; Indels 76; Gaps 8;

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DB 77 RCCEFTIYGGCGNORFESLEBCKKMCYRDANRIKTTLOQKDPFCFLR--EDPGI 133
QY 106 CGSTKTYFPNLISMTCKEFPSCGCHRNRIENRFPDEATCMGFC----- 149
DB 134 CRGYITRYVYNNQTKQCEKRFYGGCLGNM--NNFETLEBCKNICEDGPNQFOVDNYGTOL 191
QY 150 -----APKCI-----PSFCYSPDEGLCSANTRYYPNRYTCAFTYTGCG 192
DB 192 NNVNNSLTQSTKVPSELFEHGPSWCLTPADNGLCRANENRFRYNSVIGKCRPFKSGCG 251
QY 193 GNDNPFVSRDECKRACAKAL-----KKKKMPKLRPA 224
DB 252 GHNENFTSKQECIRACKGKGFIRISKGLIKTKRKRKQKORVXIA 295

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DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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GN Name=TPPI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.

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OX NCBI_TaxId=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Boutine S., Stoneking T., Phillips A.,
RT "The sequence of Homo sapiens BAC clone RP11-432D12."
RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.H.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Wilson R.K.;
RL Submitted (Apr-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 3 BPT/Kunitz inhibitor domains.
CC EMBL, AC007319; AA14807.1; -; Genomic_DNA.
CC GO, GO:0005576; C:extracellular region; IEA.
CC GO, GO:000414; F:proteinase inhibitor activity; IEA.
CC GO, GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
CC GO, GO:0007596; P:blood coagulation; IEA.
KW Hypothetical protein.
SQ SEQUENCE 304 AA; 35015 MW; 5281B32B758B44FB CRC64;

Query Match      29.7%; Score 388; DB 2; Length 304;
Best Local Similarity 30.3%; Pred. No. 4,3e-27;
Matches 86; Conservative 37; Mismatches 85; Indels 76; Gaps 8;

QY 12 LLLFLTEALGDAAB-----PTGNABICLLPDPGCRALLRLYYDRYT 58
DB 17 LLLNLAPAPLNDSEBDEHTIITDTLPPLKLMHSPCAFKADGCKAIMRFFNIPT 76
QY 59 QSCRQPLVGGCGEGNANFYTWACDCAWR-----IKYKVCRLQVSDQ-- 105
DB 77 RCCEFTIYGGCGNORFESLEBCKKMCYRDANRIKTTLOQKDPFCFLR--EDPGI 133
QY 106 CGSTKTYFPNLISMTCKEFPSCGCHRNRIENRFPDEATCMGFC----- 149
DB 134 CRGYITRYVYNNQTKQCEKRFYGGCLGNM--NNFETLEBCKNICEDGPNQFOVDNYGTOL 191
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DB 192 NNVNNSLTQSTKVPSELFEHGPSWCLTPADNGLCRANENRFRYNSVIGKCRPFKSGCG 251
QY 193 GNDNPFVSRDECKRACAKAL-----KKKKMPKLRPA 224
DB 252 GHNENFTSKQECIRACKGKGFIRISKGLIKTKRKRKQKORVXIA 295

RESULT 14
ID TPPI1_RABIT STANDARD; PRT; 300 AA.
AC P19761; Q28828;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Tissue factor pathway inhibitor precursor (TFPI) (Lipoprotein-
DE associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor
DE (BPT).
GN Name=TPPI;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxId=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=91057146; PubMed=2136251;
Weselschmidt R.L., Girard T.J., Broze G.J. Jr.;

```

RT "cDNA sequence of rabbit lipoprotein-associated coagulation  
 RT inhibitor.";  
 RT Nucleic Acids Res. 18:6440-6440(1990).  
 RN [2]  
 RP SEQUENCE REVISION TO 72; 211 AND 218.  
 RC TISSUE=Liver;  
 RX MEDLINE=92335027; PubMed=1630940;  
 RA Warn-Cramer B.J., Broze G.J. Jr., Komives E.A.,  
 RT "cDNA sequence of rabbit tissue factor pathway inhibitor.";  
 RL Nucleic Acids Res. 20:3548-3548(1992).  
 RP [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;  
 RX MEDLINE=93276427; PubMed=8503123; DOI=10.1016/0049-3848(93)90059-W;  
 RA Belarous J.A., Kupchawamy M.N., Birkhoff J.J., Bajaj S.P.,  
 RT "Revised cDNA sequence of rabbit tissue factor pathway inhibitor.";  
 RL Thromb. Res. 69:547-553(1993).  
 CC -1- FUNCTION: Inhibits factor X (X(a)) directly and, in a Xa-dependent  
 CC way, inhibits VIIa/tissue factor activity, presumably by forming a  
 CC quaternary Xa/LACI/VIIa/TF complex. It possesses an antithrombotic  
 CC action and also the ability to associate with lipoproteins in  
 CC plasma.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- DOMAIN: This inhibitor contains three inhibitory domains. The  
 CC first domain interacts with VIIa and TF, the second one with Xa  
 CC (By similarity).  
 CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.  
 CC -----  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 DR EMBL: X54708; CAA38515.1; ALT SEQ; mRNA.  
 DR EMBL: S61902; AAB36836.1; -, mRNA.  
 DR PIR: I46937; I46937.  
 DR HSRP: P10646; ITRX.  
 DR SMR: P19761; 117-173, 207-266.  
 DR InterPro: IPR002223; Prot\_inh\_Kunz-m.  
 DR InterPro: IPR008296; Prot\_inh\_TFPI.  
 DR Pfam: PF00014; Kunitz\_BPTI\_3.  
 DR PIRSF: PIRSF001620; TFPI\_1.  
 DR PRINTS: PR00759; BASICPTASE.  
 DR ProDom: PD000222; Prot\_inh\_Kunz-m; 3.  
 DR PROSITE: PS00280; BPTI\_KUNITZ\_1; 3.  
 DR PROSITE: PS0279; BPTI\_KUNITZ\_2; 3.  
 KW Blood coagulation; Glycoprotein; Protease inhibitor; Repeat;  
 KW Serine protease inhibitor; Signal.  
 FT SIGNAL 1 24  
 FT CHAIN 1 300 Tissue factor pathway inhibitor.  
 FT DOMAIN 50 170 BPTI/Kunitz inhibitor 1.  
 FT DOMAIN 121 171 BPTI/Kunitz inhibitor 2.  
 FT DOMAIN 213 263 BPTI/Kunitz inhibitor 3.  
 FT SITE 60 61 Reactive bond (By similarity).  
 FT SITE 131 132 Reactive bond (By similarity).  
 FT SITE 223 224 Reactive bond (By similarity).  
 FT CARBOHYD 141 141 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 191 191 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 252 252 N-linked (GlcNAc...) (Potential).  
 FT DISULFID 50 100 By similarity.  
 FT DISULFID 59 83 By similarity.  
 FT DISULFID 75 96 By similarity.  
 FT DISULFID 121 171 By similarity.  
 FT DISULFID 130 154 By similarity.  
 FT DISULFID 146 167 By similarity.  
 FT DISULFID 263 263 By similarity.  
 FT DISULFID 222 246 By similarity.  
 FT DISULFID 238 259 By similarity.  
 FT CONFLICT 31 31 Missing (in Ref. 3).  
 FT CONFLICT 269 272 PKSI -> RNLS (in Ref. 3).  
 FT SEQUENCE 300 AA; 34436 MW; A08DE36537708CA6 CRC64;

Query Match 29.7%; Score 387.5; DB 1; Length 300;  
 Best Local Similarity 30.7%; Pred. No. 4.7e-27;  
 Matches 89; Conservative 31; Mismatches 73; Indels 97; Gaps 8;  
 QY 12 LLLPTREALGDAAOB-----PTGNNAICLLPLDYGCRLALLRYVD 55  
 DB 13 LLLGLVPAVSSAAEDBEFTYITDIKPPQLQPTIS---FCMKVDDGFCRAIYIKRFFN 69  
 QY 56 RYTOGCRQFLYGGCGGNANFPYWEACDCAWR-----IEKVPRV 95  
 DB 70 ILTHQCEPIYGGCGGNENRFFSLBCKBKCAVDYPKMTTKLTPQKGKDPFCFLBSPGI 129  
 QY 96 CRLQVSDQCGSGIEKTPFNLSMTCKPFSGGCHRRRIERPFDEATCMFC----- 149  
 DB 130 CR-----GYITRFYNNQSKQCFYKGGCLGML--NNFSLBCKKNTCENPTSD 177  
 QY 150 -----APKXI-----PSPCYGKDEGLSANTRYYPNRYRT 182  
 DB 178 FOVDHRTQLTNTVNTLINOPTKAPRRNAFHGSPCLPPADRGLOANEIRFFYNATISK 237  
 QY 183 CDAPFTYGGGNDNPNVSRBDCRACAYAL-----KXKCKAP 219  
 DB 228 CRPFYSGGGGNENNFSTKACITACKKGFIPKSIKGLIKTKRKKKQCP 287

RESULT 15  
 ID 093424 CYPCA PRELIMINARY; PRT; 287 AA.  
 AC 093424;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 OS Cyprinus carpio (Common carp).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ruteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;  
 OC Cyprinidae; Cyprinus.  
 OC NCBI\_TaxId=7962;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Liver;  
 RA Gracey A.Y.;  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.  
 DR EMBL: AF008648; AAC19410.1; -, mRNA.  
 DR HSRP: P31713; ISHP.  
 DR GO: GO:0005576; C:extracellular region; IEA.  
 DR GO: GO:0010414; F:protease inhibitor activity; IEA.  
 DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.  
 DR GO: GO:0007536; F:blood coagulation; IEA.  
 DR InterPro: IPR002223; Prot\_inh\_Kunz-m.  
 DR InterPro: IPR008296; Prot\_inh\_TFPI.  
 DR Pfam: PF00014; Kunitz\_BPTI\_3.  
 DR PIRSF: PIRSF001620; TFPI\_1.  
 DR PRINTS: PR00759; BASICPTASE.  
 DR ProDom: PD000222; Prot\_inh\_Kunz-m; 3.  
 DR SMART: SM00131; KU; 3.  
 DR PROSITE: PS00280; BPTI\_KUNITZ\_1; 3.  
 DR PROSITE: PS0279; BPTI\_KUNITZ\_2; 3.  
 KW Hypothetical protein.  
 KW SEQUENCE 287 AA; 33093 MW; DF69B3D767181158 CRC64;  
 Query Match 29.6%; Score 387; DB 2; Length 287;  
 Best Local Similarity 35.0%; Pred. No. 5e-27;  
 Matches 85; Conservative 23; Mismatches 71; Indels 64; Gaps 7;  
 QY 36 CLLPDYGPCRALLIRYDRYTOGCRQFLYGGCGGNANFPYWEACDCAWR-RLEKVPK 94  
 DB 42 CALKQDBGPCALXKRFYFDYDTCBSPFYGGCGGNENRFFSLBCKBKCAVDYPKMTTKLTPQKGKDPFCFLBSPGI 100  
 QY 95 VCRLQVSDQCGSGIEKTPFNLSMTCKPFSGGCHRRRIERPFDEATCMFCAP 151  
 DB 101 -COL-----DDEPGPCRLGVPRYFPDFKSOBCKRFFYGGCGFN--ANNFTIYKCHERCLP 153



Qy	152	-----KK-----	IPFCY	159
Db	154	ALNNMERNAPLKPEBBEAKPTEPLAKHVEAPLNASHLPWQRMSKPSAKKPRLNRPKLCp		213
Qy	160	SPRDEGLCSANVTYYYFNPRYRTCDAPTYTGCGGNDNNFVSRREDCKRACAKALKKKKMP		219
Db	214	SPIDRGNCSGSEGRMYNPTTKRCOMFHSGCCGNNNNFVKGDCIKMCRDLRRKILRL		273
Qy	220	KLR	222	
Db	274	KLR	276	

Search completed: March 9, 2006, 19:56:47  
 Job time : 232 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 9, 2006, 19:57:04 ; Search time 47 Seconds

(without alignments)  
413.378 Million cell updates/sec

Title: US-10-800-057-2

Perfect score: 1306

Sequence: 1 MDPARPLGSLILFLTEAA.....KMPKLRPASRIKRIKKQF 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/1aa/5 COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/6 COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/7 COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/8 COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/9 COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	ID	Description
1	1306	100.0	235 1	US-08-147-710-2 Sequence 2, Appl1
2	1306	100.0	235 1	US-08-458-090-2 Sequence 2, Appl1
3	1306	100.0	235 1	US-08-457-887-2 Sequence 2, Appl1
4	1306	100.0	235 2	US-08-817-145-3 Sequence 3, Appl1
5	1306	100.0	235 2	US-09-702-705-332 Sequence 332, App
6	1306	100.0	235 2	US-09-736-457-332 Sequence 332, App
7	1306	100.0	235 2	US-09-614-1248-332 Sequence 332, App
8	1306	100.0	235 2	US-09-904-621-2 Sequence 2, Appl1
9	1306	100.0	235 2	US-09-671-325-332 Sequence 332, App
10	1306	100.0	235 2	US-09-589-184-332 Sequence 332, App
11	1306	100.0	235 2	US-09-658-824-332 Sequence 332, App
12	1306	100.0	235 2	US-09-949-016-6735 Sequence 6735, App
13	1306	100.0	235 2	US-10-017-754-332 Sequence 332, App
14	1306	100.0	235 2	US-09-651-563-332 Sequence 332, App
15	1306	100.0	235 2	US-09-519-642-332 Sequence 332, App
16	1306	100.0	235 2	US-09-949-016-7058 Sequence 7058, App
17	1200	91.9	213 1	US-08-796-850-2 Sequence 2, Appl1
18	1200	91.9	213 1	US-09-766-778-2 Sequence 2, Appl1
19	1200	91.9	213 2	US-10-086-176A-6 Sequence 6, Appl1
20	394.5	30.2	291 2	US-10-000-489-48 Sequence 48, Appl1
21	393.5	30.1	291 1	US-10-000-489-52 Sequence 52, Appl1
22	388	29.7	304 1	US-08-026-145-2 Sequence 2, Appl1
23	388	29.7	304 1	US-08-446-646-9 Sequence 9, Appl1
24	388	29.7	304 1	US-08-676-125A-18 Sequence 18, Appl1
25	388	29.7	304 1	US-09-136-012A-18 Sequence 18, Appl1
26	388	29.7	304 2	US-08-676-124-1 Sequence 1, Appl1
27	388	29.7	304 2	US-08-208-264A-25 Sequence 25, Appl1

28	388	29.7	304 2	US-09-414-878-1 Sequence 1, Appl1
29	388	29.7	304 2	US-09-240-136-1 Sequence 1, Appl1
30	388	29.7	304 2	US-09-421-097-25 Sequence 25, Appl1
31	388	29.7	304 2	US-09-638-770A-1 Sequence 1, Appl1
32	388	29.7	304 2	US-09-054-272-16 Sequence 16, Appl1
33	388	29.7	304 2	US-10-167-351-1 Sequence 1, Appl1
34	388	29.7	304 6	US-09-949-016-7400 Patent No. 5466783
35	388	29.7	304 2	US-09-437-841-9 Sequence 7400, App
36	387.5	29.7	276 1	US-08-286-521-9 Sequence 9, Appl1
37	387.5	29.7	276 1	US-08-436-175-9 Sequence 9, Appl1
38	387.5	29.7	276 1	US-08-854-764-3 Sequence 9, Appl1
39	387.5	29.7	276 2	US-08-943-682-9 Sequence 9, Appl1
40	387.5	29.7	276 2	US-09-741-106-9 Sequence 9, Appl1
41	387.5	29.7	276 4	PCT-US95-09377-3 Sequence 9, Appl1
42	387.5	29.7	276 4	PCT-US95-09464-9 Sequence 9, Appl1
43	384.5	29.4	213 6	US-08-796-850-1 Patent No. 5466783
44	384.5	29.4	276 1	US-08-796-850-1 Sequence 1, Appl1
45	384.5	29.4	276 1	US-08-796-850-1 Sequence 1, Appl1

## ALIGNMENTS

RESULT 1  
US-08-147-710-2  
; Sequence 2, Application US/08147710  
; Patent No. 5455338  
; GENERAL INFORMATION:  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Kistel, Walter  
; APPLICANT: Foster, Donald C.  
; TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS AND  
; TITLE OR INVENTION: METHODS RELATING THERETO  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSER: ZymoGenetics, Inc.  
; STREET: 4225 Roosevelt Way, N.E.  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/147,710  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, Gary E  
; REGISTRATION NUMBER: 31-684  
; REFERENCE/DOCKET NUMBER: 93-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-547-8080 ext 322  
; TELEFAX: 206-548-2329  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 235 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-147-710-2

Query Match 100.0%; Score 1306; DB 1; Length 235;  
Best local Similarity 100.0%; Pred. No. 2e-123;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGSLILFLTEAAAGPAGPAGNAEICLPLDYGPCALLRYYDRTOS 60  
DB 1 MDPARPLGSLILFLTEAAAGPAGPAGNAEICLPLDYGPCALLRYYDRTOS 60

QY 61 CROPLYGCGEGNANNFYTWACDCAKALKKKKMPKLPASIRIRIRKKQF 120  
DB 61 CROPLYGCGEGNANNFYTWACDCAKALKKKKMPKLPASIRIRIRKKQF 120  
QY 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKPIPSFCYSPDCEGCSANVTTRYFNPRY 180  
DB 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKPIPSFCYSPDCEGCSANVTTRYFNPRY 180  
QY 181 RTCDATYTYGCGGNDNNFVSRDCKRAKALKKKKMPKLPASIRIRIRKKQF 235  
DB 181 RTCDATYTYGCGGNDNNFVSRDCKRAKALKKKKMPKLPASIRIRIRKKQF 235  
RESULT 2  
US-08-458-090-2  
Sequence 2, Application US/08458090  
Patent No. 5728674  
GENERAL INFORMATION:  
APPLICANT: Sprecher, Cindy A.  
APPLICANT: Kistel, Walter  
TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS AND  
TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS AND  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Zymogenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458, 090  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, Gary E  
REGISTRATION NUMBER: 31-648  
REFERENCE/DOCKET NUMBER: 93-1402  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6673  
TELEFAX: 206-442-6678  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-458-090-2  
Query Match 100.0%; Score 1306; DB 1; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2e-123;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 181 RTCDATYTYGCGGNDNNFVSRDCKRAKALKKKKMPKLPASIRIRIRKKQF 235  
RESULT 3  
US-08-457-887-2  
Sequence 2, Application US/08457887  
Patent No. 5914315  
GENERAL INFORMATION:  
APPLICANT: Sprecher, Cindy A.  
APPLICANT: Kistel, Walter  
TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS AND  
TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS AND  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Zymogenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/457,887  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, Gary E  
REGISTRATION NUMBER: 31-648  
REFERENCE/DOCKET NUMBER: 93-1401  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6678  
TELEFAX: 206-442-6673  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-457-887-2  
Query Match 100.0%; Score 1306; DB 1; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2e-123;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGISLILFLTEALGDAQAQEPYGNNAEICLPLDYGPCRALLLRYYDRYQS 60  
DB 1 MDPARPLGISLILFLTEALGDAQAQEPYGNNAEICLPLDYGPCRALLLRYYDRYQS 60  
QY 61 CROPLYGCGEGNANNFYTWACDCAKALKKKKMPKLPASIRIRIRKKQF 120  
DB 61 CROPLYGCGEGNANNFYTWACDCAKALKKKKMPKLPASIRIRIRKKQF 120  
QY 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKPIPSFCYSPDCEGCSANVTTRYFNPRY 180  
DB 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKPIPSFCYSPDCEGCSANVTTRYFNPRY 180  
QY 181 RTCDATYTYGCGGNDNNFVSRDCKRAKALKKKKMPKLPASIRIRIRKKQF 235  
DB 181 RTCDATYTYGCGGNDNNFVSRDCKRAKALKKKKMPKLPASIRIRIRKKQF 235  
RESULT 4  
US-08-817-145-3  
Sequence 3, Application US/08817145  
Patent No. 6025339  
GENERAL INFORMATION:  
APPLICANT: Utsomi, Jun  
APPLICANT: Sudo, Tetsuo

APPLICANT: TANAKA, Yasuhiko  
APPLICANT: MATSUI, Mizuo  
TITLE OF INVENTION: THERAPEUTIC AGENT FOR OPHTHALMIC  
DISEASES  
TITLE OF INVENTION: DISEASES  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESSES:  
ADDRESSES: Birch, Stewart, Kolaesch & Birch, LLP.  
STREET: P.O. Box 747  
CITY: Falls Church  
STATE: VA  
COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,145  
FILING DATE: 02-JUL-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: MURPHY JR., Gerald M.  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 760-230P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-205-8000  
TELEFAX: 703-205-8050  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-817-145-3

Query Match 100.0%; Score 1306; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2e-123;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 181 RTCDAFTYTCGGNDNNFVSRDCKRAKAKLKKKKKMPKLPASIRIRIRKKQF 235

RESULT 5  
US-09-702-705-332  
Sequence 332, Application US/09702705  
Patent No. 6504010  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Bangur, Chaltanya S.  
APPLICANT: Lodes, Michael A.  
APPLICANT: Fanger, Gary  
APPLICANT: Vedvick, Tom  
APPLICANT: Carter, Darrick  
APPLICANT: Retter, Marc  
APPLICANT: Mannion, Jane  
APPLICANT: Fan, Liqun  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.478C14  
CURRENT APPLICATION NUMBER: US/09/702,705  
CURRENT FILING DATE: 2000-10-30  
NUMBER OF SEQ ID NOS: 1833  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 332  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-702-705-332

Query Match 100.0%; Score 1306; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2e-123;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CRQFLYGGCGEANNFYTWACDCAWRIEKVPKVCRLQVSDDCGEGSTKCYFNLSSM 120  
DB 61 CRQFLYGGCGEANNFYTWACDCAWRIEKVPKVCRLQVSDDCGEGSTKCYFNLSSM 120  
QY 121 TCEKFFSGGCHNRRINRPPDRTCMGFCAPKKIISFCYSPDDEGLCSANTVRYFNPRY 180  
DB 121 TCEKFFSGGCHNRRINRPPDRTCMGFCAPKKIISFCYSPDDEGLCSANTVRYFNPRY 180  
QY 181 RTCDAFTYTCGGNDNNFVSRDCKRAKAKLKKKKKMPKLPASIRIRIRKKQF 235  
DB 181 RTCDAFTYTCGGNDNNFVSRDCKRAKAKLKKKKKMPKLPASIRIRIRKKQF 235

RESULT 6  
US-09-736-457-332  
Sequence 332, Application US/09736457  
Patent No. 6509448  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Bangur, Chaltanya S.  
APPLICANT: Lodes, Michael A.  
APPLICANT: Fanger, Gary  
APPLICANT: Vedvick, Tom  
APPLICANT: Carter, Darrick  
APPLICANT: Retter, Marc  
APPLICANT: Mannion, Jane  
APPLICANT: Fan, Liqun  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.478C15  
CURRENT APPLICATION NUMBER: US/09/736,457  
CURRENT FILING DATE: 2000-12-13  
NUMBER OF SEQ ID NOS: 1864  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 332  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-736-457-332

Query Match 100.0%; Score 1306; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2e-123;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGSIILLFLTEALGDAOEPGNNABICLLPLDYGPCRALLLRYYYDRYTOS 60  
DB 1 MDPARPLGSIILLFLTEALGDAOEPGNNABICLLPLDYGPCRALLLRYYYDRYTOS 60  
QY 61 CRQFLYGGCGEANNFYTWACDCAWRIEKVPKVCRLQVSDDCGEGSTKCYFNLSSM 120  
DB 61 CRQFLYGGCGEANNFYTWACDCAWRIEKVPKVCRLQVSDDCGEGSTKCYFNLSSM 120

Qy 121 TCEKFSGGCHNRNLENRPDEATCMGFCAPKKIPSCYSPKDEGLCSANVTYYFNPRY 180  
Db 121 TCEKFSGGCHNRNLENRPDEATCMGFCAPKKIPSCYSPKDEGLCSANVTYYFNPRY 180  
Qy 181 RTCDATYTGCGGNDNNFVSRDECKRACAKALKKKKKMPLRPAASIRIRKKOF 235  
Db 181 RTCDATYTGCGGNDNNFVSRDECKRACAKALKKKKKMPLRPAASIRIRKKOF 235

RESULT 7  
US-09-614-124B-332  
Sequence 332, Application US/09614124B  
Patent No. 6630574  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Lodges, Michael A.  
APPLICANT: Ranger, Gary  
APPLICANT: Vedvick, Tom  
APPLICANT: Carter, Darlick  
APPLICANT: Retter, Marc  
APPLICANT: Mannion, Jane  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
FILE REFERENCE: 210121.478C9  
CURRENT APPLICATION NUMBER: US/09/614,124B  
CURRENT FILING DATE: 2001-07-11  
NUMBER OF SEQ ID NOS: 1668  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 332  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-614-124B-332

Query Match 100.0%; Score 1306; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2e-123;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDPARPLGSLILLFLTEALGDAAQEPYGNNAEICLLPLDYGPCRALLLRYYYDRYTOS 60  
Db 1 MDPARPLGSLILLFLTEALGDAAQEPYGNNAEICLLPLDYGPCRALLLRYYYDRYTOS 60  
Qy 61 CROFLYGGCEGNANNFYWEACDDACWRIEKVPKVCRLQVSYDDQCEGSTKCYFNLISM 120  
Db 61 CROFLYGGCEGNANNFYWEACDDACWRIEKVPKVCRLQVSYDDQCEGSTKCYFNLISM 120  
Qy 121 TCEKFSGGCHNRNLENRPDEATCMGFCAPKKIPSCYSPKDEGLCSANVTYYFNPRY 180  
Db 121 TCEKFSGGCHNRNLENRPDEATCMGFCAPKKIPSCYSPKDEGLCSANVTYYFNPRY 180  
Qy 181 RTCDATYTGCGGNDNNFVSRDECKRACAKALKKKKKMPLRPAASIRIRKKOF 235  
Db 181 RTCDATYTGCGGNDNNFVSRDECKRACAKALKKKKKMPLRPAASIRIRKKOF 235

RESULT 8  
US-09-904-621-2  
Sequence 2, Application US/09904621  
Patent No. 6656746  
GENERAL INFORMATION:  
APPLICANT: Sprecher, Cindy A.  
APPLICANT: Kiesel, Walter  
APPLICANT: Foster, Donald C.  
TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS  
TITLE OF INVENTION: AND  
FILE REFERENCE: 93-14D3  
CURRENT APPLICATION NUMBER: US/09/904,621  
CURRENT FILING DATE: 2001-07-13  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/265,627  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 5,455,338

PRIOR FILING DATE: EARLIER FILING DATE: 1993-11-05  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-904-621-2

Query Match 100.0%; Score 1306; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2e-123;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDPARPLGSLILLFLTEALGDAAQEPYGNNAEICLLPLDYGPCRALLLRYYYDRYTOS 60  
Db 1 MDPARPLGSLILLFLTEALGDAAQEPYGNNAEICLLPLDYGPCRALLLRYYYDRYTOS 60  
Qy 61 CROFLYGGCEGNANNFYWEACDDACWRIEKVPKVCRLQVSYDDQCEGSTKCYFNLISM 120  
Db 61 CROFLYGGCEGNANNFYWEACDDACWRIEKVPKVCRLQVSYDDQCEGSTKCYFNLISM 120  
Qy 121 TCEKFSGGCHNRNLENRPDEATCMGFCAPKKIPSCYSPKDEGLCSANVTYYFNPRY 180  
Db 121 TCEKFSGGCHNRNLENRPDEATCMGFCAPKKIPSCYSPKDEGLCSANVTYYFNPRY 180  
Qy 181 RTCDATYTGCGGNDNNFVSRDECKRACAKALKKKKKMPLRPAASIRIRKKOF 235  
Db 181 RTCDATYTGCGGNDNNFVSRDECKRACAKALKKKKKMPLRPAASIRIRKKOF 235

RESULT 9  
US-09-671-325-332  
Sequence 332, Application US/09671325  
Patent No. 6667154  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Lodges, Michael A.  
APPLICANT: Ranger, Gary  
APPLICANT: Vedvick, Tom  
APPLICANT: Carter, Darlick  
APPLICANT: Retter, Marc  
APPLICANT: Mannion, Jane  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.478C12  
CURRENT APPLICATION NUMBER: US/09/671,325  
CURRENT FILING DATE: 2000-09-26  
NUMBER OF SEQ ID NOS: 1825  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 332  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-671-325-332

Query Match 100.0%; Score 1306; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2e-123;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDPARPLGSLILLFLTEALGDAAQEPYGNNAEICLLPLDYGPCRALLLRYYYDRYTOS 60  
Db 1 MDPARPLGSLILLFLTEALGDAAQEPYGNNAEICLLPLDYGPCRALLLRYYYDRYTOS 60  
Qy 61 CROFLYGGCEGNANNFYWEACDDACWRIEKVPKVCRLQVSYDDQCEGSTKCYFNLISM 120  
Db 61 CROFLYGGCEGNANNFYWEACDDACWRIEKVPKVCRLQVSYDDQCEGSTKCYFNLISM 120  
Qy 121 TCEKFSGGCHNRNLENRPDEATCMGFCAPKKIPSCYSPKDEGLCSANVTYYFNPRY 180  
Db 121 TCEKFSGGCHNRNLENRPDEATCMGFCAPKKIPSCYSPKDEGLCSANVTYYFNPRY 180

Oy 181 RTCDAFYTGCGGNNNFVSRDCRACAKALKKKKKMPKJLPASIRIRIRKKOF 235  
Db 181 RTCDAFYTGCGGNNNFVSRDCRACAKALKKKKKMPKJLPASIRIRIRKKOF 235

RESULT 10  
US-09-589-184-332  
Sequence 332, Application US/09589184  
Patent No. 6686447  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Bangur, Chaityanya S.  
APPLICANT: Lodes, Michael A.  
APPLICANT: Panger, Gary  
APPLICANT: Vedrick, Tom  
APPLICANT: Carter, Darlick  
APPLICANT: Retter, Marc  
APPLICANT: Mannion, Jane  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
FILE REFERENCE: 210121.478C8  
CURRENT APPLICATION NUMBER: US/09/589,184  
CURRENT FILING DATE: 2000-06-05  
NUMBER OF SEQ ID NOS: 827  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 332  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-589-184-332

Query Match 100.0%; Score 1306; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2e-123;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 MDPAPPLGISLILFLTEALGDAAPPTGNNAEICLPLDYGPCRALIRYYDRYTS 60  
Db 1 MDPAPPLGISLILFLTEALGDAAPPTGNNAEICLPLDYGPCRALIRYYDRYTS 60  
Oy 61 CRQPLYGCGEGNANFYTWACDDACWRIEKVPKVCRLQVSDDCGEGSTERYFNLSSM 120  
Db 61 CRQPLYGCGEGNANFYTWACDDACWRIEKVPKVCRLQVSDDCGEGSTERYFNLSSM 120  
Oy 121 TCEKPFSGGCHNRRIENRPPDEATCMGFCAPKIKIPSCYSPDEGLCSANVTRYFNPXY 180  
Db 121 TCEKPFSGGCHNRRIENRPPDEATCMGFCAPKIKIPSCYSPDEGLCSANVTRYFNPXY 180  
Oy 181 RTCDAFYTGCGGNNNFVSRDCRACAKALKKKKKMPKJLPASIRIRIRKKOF 235  
Db 181 RTCDAFYTGCGGNNNFVSRDCRACAKALKKKKKMPKJLPASIRIRIRKKOF 235

RESULT 11  
US-09-658-824-332  
Sequence 332, Application US/09658824  
Patent No. 6746846  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Bangur, Chaityanya S.  
APPLICANT: Lodes, Michael A.  
APPLICANT: Panger, Gary  
APPLICANT: Vedrick, Tom  
APPLICANT: Carter, Darlick  
APPLICANT: Retter, Marc  
APPLICANT: Mannion, Jane  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
FILE REFERENCE: 210121.478C11  
CURRENT APPLICATION NUMBER: US/09/658,824  
CURRENT FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 1788  
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 332  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-658-824-332

Query Match 100.0%; Score 1306; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2e-123;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 MDPAPPLGISLILFLTEALGDAAPPTGNNAEICLPLDYGPCRALIRYYDRYTS 60  
Db 1 MDPAPPLGISLILFLTEALGDAAPPTGNNAEICLPLDYGPCRALIRYYDRYTS 60  
Oy 61 CRQPLYGCGEGNANFYTWACDDACWRIEKVPKVCRLQVSDDCGEGSTERYFNLSSM 120  
Db 61 CRQPLYGCGEGNANFYTWACDDACWRIEKVPKVCRLQVSDDCGEGSTERYFNLSSM 120  
Oy 121 TCEKPFSGGCHNRRIENRPPDEATCMGFCAPKIKIPSCYSPDEGLCSANVTRYFNPXY 180  
Db 121 TCEKPFSGGCHNRRIENRPPDEATCMGFCAPKIKIPSCYSPDEGLCSANVTRYFNPXY 180  
Oy 181 RTCDAFYTGCGGNNNFVSRDCRACAKALKKKKKMPKJLPASIRIRIRKKOF 235  
Db 181 RTCDAFYTGCGGNNNFVSRDCRACAKALKKKKKMPKJLPASIRIRIRKKOF 235

RESULT 12  
US-09-949-016-6735  
Sequence 6735, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6735  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-6735

Query Match 100.0%; Score 1306; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2e-123;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MDPAPPLGISLILFLTEALGDAAPPTGNNAEICLPLDYGPCRALIRYYDRYTS 60  
Oy 61 CRQPLYGCGEGNANFYTWACDDACWRIEKVPKVCRLQVSDDCGEGSTERYFNLSSM 120  
Db 61 CRQPLYGCGEGNANFYTWACDDACWRIEKVPKVCRLQVSDDCGEGSTERYFNLSSM 120  
Oy 121 TCEKPFSGGCHNRRIENRPPDEATCMGFCAPKIKIPSCYSPDEGLCSANVTRYFNPXY 180  
Db 121 TCEKPFSGGCHNRRIENRPPDEATCMGFCAPKIKIPSCYSPDEGLCSANVTRYFNPXY 180  
Oy 181 RTCDAFYTGCGGNNNFVSRDCRACAKALKKKKKMPKJLPASIRIRIRKKOF 235  
Db 181 RTCDAFYTGCGGNNNFVSRDCRACAKALKKKKKMPKJLPASIRIRIRKKOF 235



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RESULT 13
US-10-017-754-332
; Sequence 332, Application US/10017754
; Patent No. 6858204
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Rector, Marc W.
; APPLICANT: Marnierakis, Margarita
; APPLICANT: Carter, Darriack
; APPLICANT: Panger, Gary R.
; APPLICANT: Vedvyck, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C18
; CURRENT APPLICATION NUMBER: US/10/017,754
; CURRENT FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 2004
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 332
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-754-332

Query Match      100.0%; Score 1306; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 2e-123;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGISTILLFLTEALGDAQEPYNNABICLLPLDYGPCRALLLRYYYDRYTS 60
DB 1 MDPARPLGISTILLFLTEALGDAQEPYNNABICLLPLDYGPCRALLLRYYYDRYTS 60
QY 61 CROPLYGCGEGNANNFTYWEACDDACWRIEKVPKVCRLQVSYDDOCESGSTEKYPFNLSSM 120
DB 61 CROPLYGCGEGNANNFTYWEACDDACWRIEKVPKVCRLQVSYDDOCESGSTEKYPFNLSSM 120
QY 121 TCEKPFSSGCHNRRIENRPPDEATCMGFCAPKKIISFCYSPDEGLCSANVTTRYFNPRY 180
DB 121 TCEKPFSSGCHNRRIENRPPDEATCMGFCAPKKIISFCYSPDEGLCSANVTTRYFNPRY 180
QY 181 RTCDAFYTYGCGGNDNNFVSREDCKRACAKALKKKKKMPKLPFASIRIRIKRKQF 235
DB 181 RTCDAFYTYGCGGNDNNFVSREDCKRACAKALKKKKKMPKLPFASIRIRIKRKQF 235

RESULT 14
US-09-651-563-332
; Sequence 332, Application US/09651563
; Patent No. 6914132
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Panger, Gary
; APPLICANT: Vedvyck, Tom
; APPLICANT: Carter, Darriack
; APPLICANT: Rector, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C10
; CURRENT APPLICATION NUMBER: US/09/651,563
; CURRENT FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 1679
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 235
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-651-563-332

Query Match      100.0%; Score 1306; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 2e-123;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGISTILLFLTEALGDAQEPYNNABICLLPLDYGPCRALLLRYYYDRYTS 60
DB 1 MDPARPLGISTILLFLTEALGDAQEPYNNABICLLPLDYGPCRALLLRYYYDRYTS 60
QY 61 CROPLYGCGEGNANNFTYWEACDDACWRIEKVPKVCRLQVSYDDOCESGSTEKYPFNLSSM 120
DB 61 CROPLYGCGEGNANNFTYWEACDDACWRIEKVPKVCRLQVSYDDOCESGSTEKYPFNLSSM 120
QY 121 TCEKPFSSGCHNRRIENRPPDEATCMGFCAPKKIISFCYSPDEGLCSANVTTRYFNPRY 180
DB 121 TCEKPFSSGCHNRRIENRPPDEATCMGFCAPKKIISFCYSPDEGLCSANVTTRYFNPRY 180
QY 181 RTCDAFYTYGCGGNDNNFVSREDCKRACAKALKKKKKMPKLPFASIRIRIKRKQF 235
DB 181 RTCDAFYTYGCGGNDNNFVSREDCKRACAKALKKKKKMPKLPFASIRIRIKRKQF 235

Search completed: March 9, 2006, 19:58:24
Job time : 48 secs
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 9, 2006, 20:08:14 ; Search time 165 Seconds  
(without alignments)  
595.090 Million cell updates/sec

Title: US-10-800-057-2

Perfect score: 1306

Sequence: 1 MDPARPLGSLILFLTEAA.....KMPKLRPASRIKIRKKQF 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:  
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2: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/prodata/1/pubpaa/US10\_PUBCOMB.pep.\*  
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6: /cgn2\_6/prodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1306	100.0	235	3	US-09-904-621-2
2	1306	100.0	235	3	US-09-736-457-332
3	1306	100.0	235	3	US-09-902-941-332
4	1306	100.0	235	3	US-09-849-626-332
5	1306	100.0	235	3	US-09-476-300-332
6	1306	100.0	235	4	US-10-017-754-332
7	1306	100.0	235	4	US-10-060-036-167
8	1306	100.0	235	4	US-10-097-340-316
9	1306	100.0	235	4	US-10-021-660-119
10	1306	100.0	235	4	US-10-113-872-332
11	1306	100.0	235	4	US-10-283-017-332
12	1306	100.0	235	4	US-10-295-027-24
13	1306	100.0	235	4	US-10-428-487-7
14	1306	100.0	235	4	US-10-211-462-52
15	1306	100.0	235	5	US-10-680-684-2
16	1306	100.0	235	5	US-10-800-057-2
17	1306	100.0	235	5	US-10-991-321-24
18	1306	100.0	235	6	US-11-050-926-316
19	1200	91.9	213	4	US-09-766-778-6
20	1200	91.9	213	4	US-10-086-176A-2
21	703.5	53.9	184	4	US-10-425-115-318379
22	464	35.5	88	5	US-09-978-418-26
23	464	35.5	88	5	US-10-485-231-26
24	394.5	30.2	291	3	US-09-992-600A-48
25	394.5	30.2	291	3	US-09-924-340-48
26	394.5	30.2	291	3	US-09-992-095B-48
27	394.5	30.2	291	3	US-09-999-570-48

28	394.5	30.2	291	4	US-10-000-489-48	Sequence 48, App1
29	394.5	30.2	291	4	US-10-000-986-48	Sequence 48, App1
30	394.5	30.2	291	4	US-10-154-678-48	Sequence 48, App1
31	394.5	30.2	291	5	US-10-838-854-48	Sequence 48, App1
32	393.5	30.1	291	3	US-09-992-600A-52	Sequence 52, App1
33	393.5	30.1	291	3	US-09-924-340-52	Sequence 52, App1
34	393.5	30.1	291	3	US-09-992-095B-52	Sequence 52, App1
35	393.5	30.1	291	3	US-09-999-570-52	Sequence 52, App1
36	393.5	30.1	291	4	US-10-000-489-52	Sequence 52, App1
37	393.5	30.1	291	4	US-10-000-986-52	Sequence 52, App1
38	393.5	30.1	291	4	US-10-154-678-52	Sequence 52, App1
39	393.5	30.1	291	5	US-10-838-854-52	Sequence 52, App1
40	388	29.7	304	4	US-10-167-351-1	Sequence 1, App1
41	388	29.7	304	4	US-10-755-544-3	Sequence 412, App
42	388	29.7	304	4	US-10-753-544-3	Sequence 3, App1
43	388	29.7	304	5	US-10-931-153-1	Sequence 1, App1
44	388	29.7	304	5	US-10-367-057-69	Sequence 69, App1
45	388	29.7	304	5	US-10-953-902A-54	Sequence 54, App1

#### ALIGNMENTS

```

RESULT 1
US-09-904-621-2
; Sequence 2, Application US/09904621
; Patent No. US20020098560A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Kistler, Walter
; APPLICANT: Foster, Donald C.
; TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS
; TITLE OF INVENTION: AND
; FILE REFERENCE: 93-14D3
; CURRENT APPLICATION NUMBER: US/09/904,621
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/265,627
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 5,455,338
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-621-2

Query Match      100.0%; Score 1306; DB 3; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.6e-116;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MDPARPLGSLILFLTEAALGDAAGPYGNNALICLPLDYGPCRALILRYRYRTOS 60
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DB      61 CGPFLYGGCGEGNANNFYTWACDCAWRIEYKPKYCRLOVSYDDOCGSTEKFFNLSM 120
QY      121 TCEKPPSGGCHNRRLENRPDPAATCMGFCAPKKIPSCYSPDEGLCSANVRYFNPRY 180
DB      121 TCEKPPSGGCHNRRLENRPDPAATCMGFCAPKKIPSCYSPDEGLCSANVRYFNPRY 180
QY      181 RTCDATYTYGCGGNDNNFYSRBDCKRAKAKLKKKKMPKLNPAIRIRIRKKQF 235
DB      181 RTCDATYTYGCGGNDNNFYSRBDCKRAKAKLKKKKMPKLNPAIRIRIRIRKKQF 235

RESULT 2
US-09-736-457-332
; Sequence 332, Application US/09736457

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/ Patent No. US20020168637A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Tonglong
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: Lodges, Michael A.
/ APPLICANT: Fanger, Gary
/ APPLICANT: Vedvick, Tom
/ APPLICANT: Carter, Darick
/ APPLICANT: Retter, Marc
/ APPLICANT: Mannion, Jane
/ APPLICANT: Fan, Liqun
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE REFERENCE: 210121.478C15
/ CURRENT APPLICATION NUMBER: US/09/736,457
/ CURRENT FILING DATE: 2000-12-13
/ NUMBER OF SEQ ID NOS: 1864
/ SOFTWARE: FaetsEQ for Windows Version 3.0
/ SEQ ID NO 332
/ LENGTH: 235
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-736-457-332
```

```
Query Match 100.0%; Score 1306; DB 3; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.6e-116;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGSLILLPLTEALGDAAGPTGNNABICLLPLDYGPCALLRLYYDRYTS 60
DB 1 MDPARPLGSLILLPLTEALGDAAGPTGNNABICLLPLDYGPCALLRLYYDRYTS 60
QY 61 CROPLYGCEGNANNTYWEACDDACWRIEKVPKVCRLQVSDVDDCEGSTEKTFPFLSSM 120
DB 61 CROPLYGCEGNANNTYWEACDDACWRIEKVPKVCRLQVSDVDDCEGSTEKTFPFLSSM 120
QY 121 TCEKFFSGGCHRRRIENRPPDEATCMGFCAPKKIPSCYSPDEGLCSANTVRYFNPRY 180
DB 121 TCEKFFSGGCHRRRIENRPPDEATCMGFCAPKKIPSCYSPDEGLCSANTVRYFNPRY 180
QY 181 RTCDAPFTYTGCGGNDNNFVSRDCRACAKALKKKKKMPKLPASIRIRIKRKOP 235
DB 181 RTCDAPFTYTGCGGNDNNFVSRDCRACAKALKKKKKMPKLPASIRIRIKRKOP 235
```

```
RESULT 3
US-09-902-941-332
/ Sequence 332, Application US/09902941
/ Patent No. US20020172952A1
/ GENERAL INFORMATION:
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Wang, Tonglong
/ APPLICANT: Matanabe, Yoshihiro
/ APPLICANT: Johnson, Jeffrey C.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Marnierakis, Margarita
/ APPLICANT: Carter, Darick
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: McNabb, Andria
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ FILE REFERENCE: 210121.478C17
/ CURRENT APPLICATION NUMBER: US/09/902,941
/ CURRENT FILING DATE: 2001-07-10
/ NUMBER OF SEQ ID NOS: 2002
/ SOFTWARE: FaetsEQ for Windows Version 4.0
/ SEQ ID NO 332
/ LENGTH: 235
/ TYPE: PRT
/ ORGANISM: Homo sapiens
```

```
US-09-902-941-332
Query Match 100.0%; Score 1306; DB 3; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.6e-116;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGSLILLPLTEALGDAAGPTGNNABICLLPLDYGPCALLRLYYDRYTS 60
DB 1 MDPARPLGSLILLPLTEALGDAAGPTGNNABICLLPLDYGPCALLRLYYDRYTS 60
QY 61 CROPLYGCEGNANNTYWEACDDACWRIEKVPKVCRLQVSDVDDCEGSTEKTFPFLSSM 120
DB 61 CROPLYGCEGNANNTYWEACDDACWRIEKVPKVCRLQVSDVDDCEGSTEKTFPFLSSM 120
QY 121 TCEKFFSGGCHRRRIENRPPDEATCMGFCAPKKIPSCYSPDEGLCSANTVRYFNPRY 180
DB 121 TCEKFFSGGCHRRRIENRPPDEATCMGFCAPKKIPSCYSPDEGLCSANTVRYFNPRY 180
QY 181 RTCDAPFTYTGCGGNDNNFVSRDCRACAKALKKKKKMPKLPASIRIRIKRKOP 235
DB 181 RTCDAPFTYTGCGGNDNNFVSRDCRACAKALKKKKKMPKLPASIRIRIKRKOP 235
```

```
RESULT 4
US-09-849-626-332
/ Sequence 332, Application US/09849626
/ Publication No. US20020197669A1
/ GENERAL INFORMATION:
/ APPLICANT: Bangur, Chaitanya
/ APPLICANT: Fanger, Gary
/ APPLICANT: Wang, Tonglong
/ APPLICANT: Switzer, Anne
/ APPLICANT: McNeill, Patricia
/ APPLICANT: Clapper, Jonathan
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE REFERENCE: 210121.478C16
/ CURRENT APPLICATION NUMBER: US/09/849,626
/ CURRENT FILING DATE: 2001-05-03
/ NUMBER OF SEQ ID NOS: 1926
/ SOFTWARE: FaetsEQ for Windows Version 3.0
/ SEQ ID NO 332
/ LENGTH: 235
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-849-626-332
```

```
Query Match 100.0%; Score 1306; DB 3; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.6e-116;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGSLILLPLTEALGDAAGPTGNNABICLLPLDYGPCALLRLYYDRYTS 60
DB 1 MDPARPLGSLILLPLTEALGDAAGPTGNNABICLLPLDYGPCALLRLYYDRYTS 60
QY 61 CROPLYGCEGNANNTYWEACDDACWRIEKVPKVCRLQVSDVDDCEGSTEKTFPFLSSM 120
DB 61 CROPLYGCEGNANNTYWEACDDACWRIEKVPKVCRLQVSDVDDCEGSTEKTFPFLSSM 120
QY 121 TCEKFFSGGCHRRRIENRPPDEATCMGFCAPKKIPSCYSPDEGLCSANTVRYFNPRY 180
DB 121 TCEKFFSGGCHRRRIENRPPDEATCMGFCAPKKIPSCYSPDEGLCSANTVRYFNPRY 180
QY 181 RTCDAPFTYTGCGGNDNNFVSRDCRACAKALKKKKKMPKLPASIRIRIKRKOP 235
DB 181 RTCDAPFTYTGCGGNDNNFVSRDCRACAKALKKKKKMPKLPASIRIRIKRKOP 235
```

```
RESULT 5
US-09-476-300-332
/ Sequence 332, Application US/09476300
/ Publication No. US20030125245A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Tongtong
/ APPLICANT: Bangur, Chaltanya S.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
/ FILE REFERENCE: 210121.478C3
/ CURRENT APPLICATION NUMBER: US/09/476,300
/ CURRENT FILING DATE: 1999-12-30
/ NUMBER OF SEQ ID NOS: 785
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 332
/ LENGTH: 235
/ TYPE: PRF
/ ORGANISM: Homo sapiens
/ US-09-476-300-332
```

```
Query Match 100.0%; Score 1306; DB 3; Length 235;
Best Local Similarity 100.0%; Pred. No. 2,6e-116;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MDPARPLGSLILLFLTEALGDAOEPYNNNAICLLPLDYGPCRALILRYYYDRYTOS 60
DB 1 MDPARPLGSLILLFLTEALGDAOEPYNNNAICLLPLDYGPCRALILRYYYDRYTOS 60
QY 61 CROFLYGCGEGNANNFYTWACDDACMRLEKVPKVCRLQVSVDDQEGSTKXFFNLSSM 120
DB 61 CROFLYGCGEGNANNFYTWACDDACMRLEKVPKVCRLQVSVDDQEGSTKXFFNLSSM 120
QY 121 TCEKFPSSGCHNRRIENRPPDEATCMGFCAPKKIPSCYSPKDEGLCSANVTRYFNPRY 180
DB 121 TCEKFPSSGCHNRRIENRPPDEATCMGFCAPKKIPSCYSPKDEGLCSANVTRYFNPRY 180
QY 181 RTCDATFTYTGCGGNDNNFVSRDCKRACAKALKKKKKMPKLPASIRIRIKKKOP 235
DB 181 RTCDATFTYTGCGGNDNNFVSRDCKRACAKALKKKKKMPKLPASIRIRIKKKOP 235
```

```
RESULT 6
US-10-017-754-332
/ Sequence 332, Application US/10017754
/ Publication No. US20030054363A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Wang, Tongtong
/ APPLICANT: Watanabe, Yoshihiro
/ APPLICANT: Johnson, Jeffrey C.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Marnerakis, Margarita
/ APPLICANT: Carter, Derrick
/ APPLICANT: Panger, Gary R.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Bangur, Chaltanya S.
/ APPLICANT: McNabb, Andria
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ FILE REFERENCE: 210121.478C18
/ CURRENT APPLICATION NUMBER: US/10/017,754
/ CURRENT FILING DATE: 2001-10-29
/ NUMBER OF SEQ ID NOS: 2004
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 332
/ LENGTH: 235
/ TYPE: PRF
/ ORGANISM: Homo sapiens
/ US-10-017-754-332
```

```
Query Match 100.0%; Score 1306; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 2,6e-116;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MDPARPLGSLILLFLTEALGDAOEPYNNNAICLLPLDYGPCRALILRYYYDRYTOS 60
DB 1 MDPARPLGSLILLFLTEALGDAOEPYNNNAICLLPLDYGPCRALILRYYYDRYTOS 60
```

```
QY 61 CROFLYGCGEGNANNFYTWACDDACMRLEKVPKVCRLQVSVDDQEGSTKXFFNLSSM 120
DB 61 CROFLYGCGEGNANNFYTWACDDACMRLEKVPKVCRLQVSVDDQEGSTKXFFNLSSM 120
QY 121 TCEKFPSSGCHNRRIENRPPDEATCMGFCAPKKIPSCYSPKDEGLCSANVTRYFNPRY 180
DB 121 TCEKFPSSGCHNRRIENRPPDEATCMGFCAPKKIPSCYSPKDEGLCSANVTRYFNPRY 180
QY 181 RTCDATFTYTGCGGNDNNFVSRDCKRACAKALKKKKKMPKLPASIRIRIKKKOP 235
DB 181 RTCDATFTYTGCGGNDNNFVSRDCKRACAKALKKKKKMPKLPASIRIRIKKKOP 235
```

```
RESULT 7
US-10-060-036-167
```

```
/ Sequence 167, Application US/10060036
/ Publication No. US20030073144A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Benson, Darin R.
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Lodes, Michael J.
/ APPLICANT: Persing, David H.
/ APPLICANT: Hepler, William T.
/ APPLICANT: Jiang, Yugu
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ FILE REFERENCE: 210121.566
/ CURRENT APPLICATION NUMBER: US/10/060,036
/ CURRENT FILING DATE: 2002-01-30
/ NUMBER OF SEQ ID NOS: 4560
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 167
/ LENGTH: 235
/ TYPE: PRF
/ ORGANISM: Homo sapiens
/ US-10-060-036-167
```

```
Query Match 100.0%; Score 1306; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 2,6e-116;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MDPARPLGSLILLFLTEALGDAOEPYNNNAICLLPLDYGPCRALILRYYYDRYTOS 60
DB 1 MDPARPLGSLILLFLTEALGDAOEPYNNNAICLLPLDYGPCRALILRYYYDRYTOS 60
QY 61 CROFLYGCGEGNANNFYTWACDDACMRLEKVPKVCRLQVSVDDQEGSTKXFFNLSSM 120
DB 61 CROFLYGCGEGNANNFYTWACDDACMRLEKVPKVCRLQVSVDDQEGSTKXFFNLSSM 120
QY 121 TCEKFPSSGCHNRRIENRPPDEATCMGFCAPKKIPSCYSPKDEGLCSANVTRYFNPRY 180
DB 121 TCEKFPSSGCHNRRIENRPPDEATCMGFCAPKKIPSCYSPKDEGLCSANVTRYFNPRY 180
QY 181 RTCDATFTYTGCGGNDNNFVSRDCKRACAKALKKKKKMPKLPASIRIRIKKKOP 235
DB 181 RTCDATFTYTGCGGNDNNFVSRDCKRACAKALKKKKKMPKLPASIRIRIKKKOP 235
```

```
RESULT 8
US-10-097-340-316
```

```
/ Sequence 316, Application US/10097340
/ Publication No. US20030087250A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: John MONAHAN
/ APPLICANT: Manjula GANNAVAPARU
/ APPLICANT: Sebastian HORSCH
/ APPLICANT: Shubhangi KAMATKAR
/ APPLICANT: Steve G. KOVATS
/ APPLICANT: Rachel E. MEYERS
/ APPLICANT: Michael MORRISSEY
/ APPLICANT: Peter OLANDT
/ APPLICANT: Ami SEN
```

```

1  APPLICANT: Peter VEIBY
2  APPLICANT: Gordon B. MILLS
3  APPLICANT: Robert C. BAST, Jr.
4  APPLICANT: Karen LU
5  APPLICANT: Rosemarie SCHMANDT
6  APPLICANT: Xumei ZHAO
7  APPLICANT: Karen GLATT
8  TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification
9  TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
10 FILE REFERENCE: M01-030
11 CURRENT APPLICATION NUMBER: US/10/097,340
12 CURRENT FILING DATE: 2002-03-14
13 PRIOR APPLICATION NUMBER: 60/276,025
14 PRIOR FILING DATE: 2001-03-14
15 PRIOR APPLICATION NUMBER: 60/325,149
16 PRIOR FILING DATE: 2001-09-26
17 PRIOR APPLICATION NUMBER: 60/276,026
18 PRIOR FILING DATE: 2001-03-14
19 PRIOR APPLICATION NUMBER: 60/324,967
20 PRIOR FILING DATE: 2001/09/26
21 PRIOR APPLICATION NUMBER: 60/311,732
22 PRIOR FILING DATE: 2001-08-10
23 PRIOR APPLICATION NUMBER: 60/325,102
24 PRIOR FILING DATE: 2001-09-26
25 PRIOR APPLICATION NUMBER: 60/323,580
26 PRIOR FILING DATE: 2001-09-19
27 NUMBER OF SEQ ID NOS: 363
28 SOFTWARE: FastSeq for Windows Version 4.0
29 SEQ ID NO 316
30 LENGTH: 235
31 TYPE: PR1
32 ORGANISM: Homo sapiens
33 US-10-097-340-316

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Query Match	100.0%	Score 1306	DB 4	Length 235
Best Local Similarity	100.0%	Pred. No. 2.6e-116		
Matches 235	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MDPARPLGLSTLLFLTEAALGDAAOEPYGNNAIECLPLDYGPCRALLLRYYDRYQS	60	
Db	1	MDPARPLGLSTLLFLTEAALGDAAOEPYGNNAIECLPLDYGPCRALLLRYYDRYQS	60	
QY	61	CROPLVGGCGEANNANFYTWEACDCAWRIEYVPKYCRLQVSDVDCGSGTEKYFNNLSM	120	
Db	61	CROPLVGGCGEANNANFYTWEACDCAWRIEYVPKYCRLQVSDVDCGSGTEKYFNNLSM	120	
QY	121	TCEKFPFGGCGGRNIENRFPDEATCMGFCAPKKIIPSCYSPKDELSGANTRYRYFNRY	180	
Db	121	TCEKFPFGGCGGRNIENRFPDEATCMGFCAPKKIIPSCYSPKDELSGANTRYRYFNRY	180	
QY	181	RTCDAFYTTGGCGGNDNPFVSRDECKRACAKLKKKKKPKLRFASIRIKRKQF	235	
Db	181	RTCDAFYTTGGCGGNDNPFVSRDECKRACAKLKKKKKPKLRFASIRIKRKQF	235	

RESULT 9  
US-10-021-660-119  
; Sequence 119, Application US/10021660  
; Publication No. US20030152926A1  
; GENERAL INFORMATION:  
; APPLICANT: Murray, Richard  
; APPLICANT: Glynn, Richard  
; APPLICANT: Watson, Susan R.  
; APPLICANT: EOS Biotechnology, Inc.  
; TITLE OF INVENTION: No. US20030152926A1el Methods of Diagnosis of Angiogenesis  
; TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis  
; FILE REFERENCE: 018501-000710US  
; CURRENT APPLICATION NUMBER: US/10/021, 660  
; CURRENT FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: US/09/784, 356  
; PRIOR FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: US 09/637, 977

```

; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PaSeq for Windows Version 3.0
; SEQ ID NO: 119
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-021-660-119

Query Matchh          100.0%; Score 1306; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 2,6e-116;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MDPARPIGLSILLILFLTEALVGDAAQEPPTGNNAEICLLPLDYGCRALLLRYTDRYQS 60
Db      1 MDPARPIGLSILLILFLTEALVGDAAQEPPTGNNAEICLLPLDYGCRALLLRYTDRYQS 60

QY      61 CRQPLVGGCGGNANNFPTWEACDDCAKRIKVPVPCVLQVSVVDQCGSGSTKRYFNNLSM 120
Db      61 CRQPLVGGCGGNANNFPTWEACDDCAKRIKVPVPCVLQVSVVDQCGSGSTKRYFNNLSM 120

QY      121 TCCEFFSGGCHRRRIENRFPDEATCMGFCAPKKIPSCVSPKDGELCSANTRYVFNRY 180
Db      121 TCCEFFSGGCHRRRIENRFPDEATCMGFCAPKKIPSCVSPKDGELCSANTRYVFNRY 180

QY      181 RTCDAPFYTGGCGGDNNFVSRBDCRAKAYALKKKKKMPKLRFAFARIKRIKKQF 235
Db      181 RTCDAPFYTGGCGGDNNFVSRBDCRAKAYALKKKKKMPKLRFAFARIKRIKKQF 235

```

```

RESULT 10
US-10-113-872-332
; Sequence 332, Application US/10113872
; Publication No. US20030170255A1
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C19
; CURRENT APPLICATION NUMBER: US/10/113.872
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 2011
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 332
; LENGTH: 235
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-113-872-332

Query Match          100.0%; Score 1306; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 2 6e-116;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MDPARPLGISILLFLTEALGDAOEPFGNNALCLPLDYGCRALLRLYYDRYTQS 60
Db      1 MDPARPLGISILLFLTEALGDAOEPFGNNALCLPLDYGCRALLRLYYDRYTQS 60

QY      61 CRQPLVGGCGGANNPFTWACDCAKRIKVRVCLQVSVDDQCGSGTIRKYPNLSM 120
Db      61 CRQPLVGGCGGANNPFTWACDCAKRIKVRVCLQVSVDDQCGSGTIRKYPNLSM 120

QY      121 TCCKPFGGCHRRRIENRPFDEATCMQFCAPKKIIPSCYSPKQEGCSANVTRYYFNPRY 180
Db      121 TCCKPFGGCHRRRIENRPFDEATCMQFCAPKKIIPSCYSPKQEGCSANVTRYYFNPRY 180

QY      181 RTCDAPFTYTCGGGNDNNFVSREDCKACAVALKKKKKMPKLRFASRIIRKIKQF 235

```

Db 181 RTCAFTYTGCGGNDNFVSRBDCRAKAKLKKKKKMPKLFASIRIRIRKQF 235

RESULT 11

US-10-283-017-332

Sequence 332, Application US/10283017

Publication No. US20030211510A1

GENERAL INFORMATION:

APPLICANT: Henderson, Robert A.

APPLICANT: Wang, Tongtong

APPLICANT: Watanabe, Yoshihiro

APPLICANT: Kales, Michael D.

APPLICANT: Sleath, Paul R.

APPLICANT: Johnson, Jeffrey C.

APPLICANT: Reiter, Marc W.

APPLICANT: Durham, Margalita

APPLICANT: Carter, Darrick

APPLICANT: Panger, Gary R.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Bangur, Chaitanya S.

APPLICANT: McNabb, Andria

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.478C20

CURRENT APPLICATION NUMBER: US/10/283,017

CURRENT FILING DATE: 2002-10-28

NUMBER OF SEQ ID NOS: 2157

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 332

LENGTH: 235

TYPE: PRT

ORGANISM: Homo sapiens

US-10-283-017-332

Query Match 100.0%; Score 1306; DB 4; Length 235;

Best Local Similarity 100.0%; Pred. No. 2.6e-116; Mismatches 0; Indels 0; Gaps 0;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDPARPLGLSILLFLTEALGDAQEPYNNABICLLPLDYGPCRALILRYRYRYS 60

Db 1 MDPARPLGLSILLFLTEALGDAQEPYNNABICLLPLDYGPCRALILRYRYRYS 60

Qy 61 CROFLYGCCEGANNFYTWBACDDACWRIEKVPKVCRLQVSDQCEGSTERYFNNLSM 120

Db 61 CROFLYGCCEGANNFYTWBACDDACWRIEKVPKVCRLQVSDQCEGSTERYFNNLSM 120

Qy 121 TCEKFPSSGCHNRLENRPDEATCMGFCAPKCIIPSCYSPROBGLCSANTRYRYFNPRY 180

Db 121 TCEKFPSSGCHNRLENRPDEATCMGFCAPKCIIPSCYSPROBGLCSANTRYRYFNPRY 180

Qy 181 RTCAFTYTGCGGNDNFVSRBDCRAKAKLKKKKKMPKLFASIRIRIRKQF 235

Db 181 RTCAFTYTGCGGNDNFVSRBDCRAKAKLKKKKKMPKLFASIRIRIRKQF 235

RESULT 12

US-10-295-027-24

Sequence 24, Application US/10295027

Publication No. US2003023250A1

GENERAL INFORMATION:

APPLICANT: Afar, Daniel

APPLICANT: Aziz, Natsaba

APPLICANT: Ginsberg, Wendy M.

APPLICANT: Glen, Kurt C.

APPLICANT: Glynn, Richard

APPLICANT: Hevezl, Peter A.

APPLICANT: Mack, David H.

APPLICANT: Murray, Richard

APPLICANT: Watson, Susan R.

APPLICANT: Eos Biotechnology, Inc.

TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and

TITLE OF INVENTION: Methods of Screening for Modulators of Cancer

FILE REFERENCE: 018501-012500US

CURRENT APPLICATION NUMBER: US/10/295,027

CURRENT FILING DATE: 2002-11-13

PRIOR APPLICATION NUMBER: US 09/663,733

PRIOR FILING DATE: 2000-09-15

PRIOR APPLICATION NUMBER: US 60/350,666

PRIOR FILING DATE: 2001-11-13

PRIOR APPLICATION NUMBER: US 60/335,394

PRIOR FILING DATE: 2001-11-15

PRIOR APPLICATION NUMBER: US 60/332,464

PRIOR FILING DATE: 2001-11-21

PRIOR APPLICATION NUMBER: US 60/334,393

PRIOR FILING DATE: 2001-11-29

PRIOR APPLICATION NUMBER: US 60/340,376

PRIOR FILING DATE: 2001-12-14

PRIOR APPLICATION NUMBER: US 60/347,211

PRIOR FILING DATE: 2002-01-08

PRIOR APPLICATION NUMBER: US 60/347,349

PRIOR FILING DATE: 2002-01-10

PRIOR APPLICATION NUMBER: US 60/355,250

PRIOR FILING DATE: 2002-02-08

PRIOR APPLICATION NUMBER: US 60/356,714

Remaining Prior Application data removed - See file Wrapper or PALM.

NUMBER OF SEQ ID NOS: 1366

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 24

LENGTH: 235

TYPE: PRT

ORGANISM: Homo sapiens

US-10-295-027-24

Query Match 100.0%; Score 1306; DB 4; Length 235;

Best Local Similarity 100.0%; Pred. No. 2.6e-116; Mismatches 0; Indels 0; Gaps 0;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDPARPLGLSILLFLTEALGDAQEPYNNABICLLPLDYGPCRALILRYRYRYS 60

Db 1 MDPARPLGLSILLFLTEALGDAQEPYNNABICLLPLDYGPCRALILRYRYRYS 60

Qy 61 CROFLYGCCEGANNFYTWBACDDACWRIEKVPKVCRLQVSDQCEGSTERYFNNLSM 120

Db 61 CROFLYGCCEGANNFYTWBACDDACWRIEKVPKVCRLQVSDQCEGSTERYFNNLSM 120

Qy 121 TCEKFPSSGCHNRLENRPDEATCMGFCAPKCIIPSCYSPROBGLCSANTRYRYFNPRY 180

Db 121 TCEKFPSSGCHNRLENRPDEATCMGFCAPKCIIPSCYSPROBGLCSANTRYRYFNPRY 180

Qy 181 RTCAFTYTGCGGNDNFVSRBDCRAKAKLKKKKKMPKLFASIRIRIRKQF 235

Db 181 RTCAFTYTGCGGNDNFVSRBDCRAKAKLKKKKKMPKLFASIRIRIRKQF 235

RESULT 13

US-10-428-487-7

Sequence 7, Application US/10428487

Publication No. US20040006780A1

GENERAL INFORMATION:

APPLICANT: RASTELLI, LUCA K.

APPLICANT: GERBER, HANS-PETER

TITLE OF INVENTION: VEGF-MODULATED GENES AND METHODS EMPLOYING THEM

FILE REFERENCE: 09800080-0103

CURRENT APPLICATION NUMBER: US/10/428,487

CURRENT FILING DATE: 2003-05-02

PRIOR APPLICATION NUMBER: 09/815,153

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,201

PRIOR FILING DATE: 2000-03-22

NUMBER OF SEQ ID NOS: 84

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 7

LENGTH: 235

TYPE: PRT

ORGANISM: Homo sapiens

US-10-428-487-7

Query Match 100.0%; Score 1306; DB 4; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2.6e-116;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGISILLPLTEALGDAOEPYNNNAEICLPLDYGPCRALLRYYDRYQS 60  
DB 1 MDPARPLGISILLPLTEALGDAOEPYNNNAEICLPLDYGPCRALLRYYDRYQS 60  
QY 61 CRQFLYGGCEGNANFYTWACDDACWRIEKVPKVCRLQVSVDDQCEGSTERYFPNLSSM 120  
DB 61 CRQFLYGGCEGNANFYTWACDDACWRIEKVPKVCRLQVSVDDQCEGSTERYFPNLSSM 120  
QY 121 TCEKFPSSGCHNRNLENRPDEATCMGFCAPKIPSPFCYSPROEGLCSANTTRYFNPRY 180  
DB 121 TCEKFPSSGCHNRNLENRPDEATCMGFCAPKIPSPFCYSPROEGLCSANTTRYFNPRY 180  
QY 181 RTCDAFYTYGCGGNDNNFVSRBDCRACAKALKKKKKMPKLPASRIRIRKKQP 235  
DB 181 RTCDAFYTYGCGGNDNNFVSRBDCRACAKALKKKKKMPKLPASRIRIRKKQP 235

RESULT 14

US-10-211-462-52  
Sequence 52, Application US/10211462  
Publication No. US20040033495A1  
GENERAL INFORMATION:  
APPLICANT: Murray, Richard  
APPLICANT: Glynn, Richard  
APPLICANT: Watson, Susan R.  
APPLICANT: Aziz, Natasha  
APPLICANT: Eos Biotechnology, Inc.  
TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and  
FILE REFERENCE: 018501-006200US  
CURRENT APPLICATION NUMBER: US/10/211,462  
CURRENT FILING DATE: 2003-02-13  
PRIOR APPLICATION NUMBER: US 09/784,356  
PRIOR FILING DATE: 2001-02-14  
PRIOR APPLICATION NUMBER: US 09/791,390  
PRIOR FILING DATE: 2001-02-22  
PRIOR APPLICATION NUMBER: US 60/310,025  
PRIOR FILING DATE: 2001-08-03  
PRIOR APPLICATION NUMBER: US 60/334,244  
PRIOR FILING DATE: 2001-11-29  
NUMBER OF SEQ ID NOS: 230  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 52  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-211-462-52

Query Match 100.0%; Score 1306; DB 4; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2.6e-116;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGISILLPLTEALGDAOEPYNNNAEICLPLDYGPCRALLRYYDRYQS 60  
DB 1 MDPARPLGISILLPLTEALGDAOEPYNNNAEICLPLDYGPCRALLRYYDRYQS 60  
QY 61 CRQFLYGGCEGNANFYTWACDDACWRIEKVPKVCRLQVSVDDQCEGSTERYFPNLSSM 120  
DB 61 CRQFLYGGCEGNANFYTWACDDACWRIEKVPKVCRLQVSVDDQCEGSTERYFPNLSSM 120  
QY 121 TCEKFPSSGCHNRNLENRPDEATCMGFCAPKIPSPFCYSPROEGLCSANTTRYFNPRY 180  
DB 121 TCEKFPSSGCHNRNLENRPDEATCMGFCAPKIPSPFCYSPROEGLCSANTTRYFNPRY 180  
QY 181 RTCDAFYTYGCGGNDNNFVSRBDCRACAKALKKKKKMPKLPASRIRIRKKQP 235  
DB 181 RTCDAFYTYGCGGNDNNFVSRBDCRACAKALKKKKKMPKLPASRIRIRKKQP 235

RESULT 15  
US-10-680-684-2

Sequence 2, Application US/10680684

Publication No. US20040253686A1

GENERAL INFORMATION:

APPLICANT: Sprecher, Cindy A.

APPLICANT: Kistel, Walter

APPLICANT: Foster, Donald C.

TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS

TITLE OF INVENTION: AND

TITLE OF INVENTION: METHODS RELATING THERETO

FILE REFERENCE: 93-1403

CURRENT APPLICATION NUMBER: US/10/680,684

CURRENT FILING DATE: 2003-10-07

PRIOR APPLICATION NUMBER: US/09/904,621

PRIOR FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: 09/265,627

PRIOR FILING DATE: PRIOR FILING DATE: 1999-03-09

PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: 5,455,338

PRIOR FILING DATE: PRIOR FILING DATE: 1993-11-05

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2

LENGTH: 235

TYPE: PRT

ORGANISM: Homo sapiens

US-10-680-684-2

Query Match 100.0%; Score 1306; DB 5; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2.6e-116;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGISILLPLTEALGDAOEPYNNNAEICLPLDYGPCRALLRYYDRYQS 60  
DB 1 MDPARPLGISILLPLTEALGDAOEPYNNNAEICLPLDYGPCRALLRYYDRYQS 60  
QY 61 CRQFLYGGCEGNANFYTWACDDACWRIEKVPKVCRLQVSVDDQCEGSTERYFPNLSSM 120  
DB 61 CRQFLYGGCEGNANFYTWACDDACWRIEKVPKVCRLQVSVDDQCEGSTERYFPNLSSM 120  
QY 121 TCEKFPSSGCHNRNLENRPDEATCMGFCAPKIPSPFCYSPROEGLCSANTTRYFNPRY 180  
DB 121 TCEKFPSSGCHNRNLENRPDEATCMGFCAPKIPSPFCYSPROEGLCSANTTRYFNPRY 180  
QY 181 RTCDAFYTYGCGGNDNNFVSRBDCRACAKALKKKKKMPKLPASRIRIRKKQP 235  
DB 181 RTCDAFYTYGCGGNDNNFVSRBDCRACAKALKKKKKMPKLPASRIRIRKKQP 235

Search completed: March 9, 2006, 20:11:33  
Job time : 167 secs



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using SW model

Run on: March 9, 2006, 20:08:54 ; Search time 23 Seconds

(without alignments)  
284,400 Million cell updates/sec

Title: US-10-800-057-2

Perfect score: 1306  
Sequence: 1 MDPARPLGSLILLFLTEBA.....KKMPKLRFPASIRIRIKRKQF 235

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:\*  
1: /cgn2\_6/prodata/1/pubppa/US08\_NEW\_PUB.pep:\*  
2: /cgn2\_6/prodata/1/pubppa/US06\_NEW\_PUB.pep:\*  
3: /cgn2\_6/prodata/1/pubppa/US07\_NEW\_PUB.pep:\*  
4: /cgn2\_6/prodata/1/pubppa/PCF\_NEW\_PUB.pep:\*  
5: /cgn2\_6/prodata/1/pubppa/US09\_NEW\_PUB.pep:\*  
6: /cgn2\_6/prodata/1/pubppa/US10\_NEW\_PUB.pep:\*  
7: /cgn2\_6/prodata/1/pubppa/US11\_NEW\_PUB.pep:\*  
8: /cgn2\_6/prodata/1/pubppa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1306	100.0	235	6	US-10-821-234-1398
2	1200	91.9	213	7	US-11-183-555-6
3	388	29.7	304	6	US-10-821-234-1540
4	384.5	29.4	276	7	US-11-183-555-5
5	180	13.8	352	7	US-11-000-463-450
6	180	13.8	352	7	US-11-000-463-922
7	180	13.8	352	7	US-11-177-506-28
8	179.5	13.7	548	7	US-11-137-465-47
9	160	12.3	94	6	US-10-821-234-1123
10	146	11.2	58	7	US-11-068-783-54
11	141	10.8	770	6	US-10-982-545-15
12	141	10.8	770	6	US-10-789-273-38
13	130	10.0	763	6	US-10-821-234-1619
14	125	9.6	353	7	US-11-137-465-44
15	125	9.6	448	7	US-11-137-465-45
16	124	9.5	99	5	US-09-978-360A-492
17	116	8.9	99	5	US-09-978-360A-618
18	107	8.2	1210	7	US-11-113-202-6
19	107	8.2	1210	7	US-11-145-566-1
20	103	7.9	23	7	US-11-183-555-4
21	97.5	7.5	1308	6	US-10-912-971-12
22	97.5	7.5	1308	6	US-11-113-202-16
23	90	6.9	317	6	US-10-620-787-21
24	88	6.7	317	6	US-10-620-787-22
25	88	6.7	963	6	US-10-995-561-923

26	88	6.7	963	6	US-10-453-372-660	Sequence 660, App
27	88	6.7	1012	6	US-10-453-372-646	Sequence 646, App
28	87	6.7	3333	6	US-10-766-317-4	Sequence 4, App1
29	86.5	6.6	3597	7	US-11-019-711-6	Sequence 6, App1
30	86.5	6.6	3600	7	US-11-019-711-2	Sequence 2, App1
31	86	6.6	1001	7	US-11-132-285-40	Sequence 40, App1
32	86	6.6	1013	6	US-10-131-826A-38	Sequence 38, App1
33	86	6.6	1013	6	US-10-973-115B-38	Sequence 38, App1
34	85.5	6.5	707	7	US-11-072-512-1162	Sequence 3162, App
35	83.5	6.4	3714	6	US-10-995-561-1015	Sequence 1015, App
36	83.5	6.4	3717	6	US-10-821-234-1076	Sequence 1076, App
37	82	6.3	4544	6	US-11-051-035-214	Sequence 214, App1
38	82	6.3	4544	7	US-11-076-427A-32	Sequence 32, App1
39	81	6.2	340	7	US-11-226-657-174	Sequence 174, App1
40	80.5	6.2	2923	7	US-11-200-822-3	Sequence 3, App1
41	79	6.0	243	6	US-10-512-103-23	Sequence 23, App1
42	79	6.0	721	7	US-11-022-478-12	Sequence 12, App1
43	78	6.0	1620	6	US-10-055-877-213	Sequence 213, App
44	78	6.0	1664	6	US-10-055-877-212	Sequence 212, App
45	77.5	5.9	365	7	US-11-108-528-56	Sequence 56, App1

#### ALIGNMENTS

```
RESULT 1
US-10-821-234-1398
; Sequence 1398, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Method for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCES: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_ssq_genes Version 1.0
; SEQ ID NO 1398
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1398

Query Match      100.0%  Score 1306; DB 6; Length 235;
Best Local Similarity 100.0%  Pred. No. 3.7e-122;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGSLILLFLTEBALGDAQEPYNNAEICLPLDYGPCRALILRYRYDRTQS 60
   |||
DB 1 MDPARPLGSLILLFLTEBALGDAQEPYNNAEICLPLDYGPCRALILRYRYDRTQS 60
   |||

QY 61 CROFLYGGCEGNNANFYTWBACDCAWRLEKYPKVCRLQVSVDDQCEGSTEKFFNLSSM 120
   |||
DB 61 CROFLYGGCEGNNANFYTWBACDCAWRLEKYPKVCRLQVSVDDQCEGSTEKFFNLSSM 120
   |||

QY 121 TCCKFPFGGCHNRIRNRPDEATCMGFCAPKKIPBFCSPDQEGCSANVRYRNPXY 180
   |||
DB 121 TCCKFPFGGCHNRIRNRPDEATCMGFCAPKKIPBFCSPDQEGCSANVRYRNPXY 180
   |||

QY 181 RTCDATYYGCGGNDNPFVSRBDCRCAKAKLKKKKMFKLFPASIRIRIKRKQF 235
   |||
DB 181 RTCDATYYGCGGNDNPFVSRBDCRCAKAKLKKKKMFKLFPASIRIRIKRKQF 235
   |||

RESULT 2
US-11-183-555-6
; Sequence 6, Application US/1183555
; Publication No. US20060025329A1
```

GENERAL INFORMATION:  
APPLICANT: Hembrough, Todd  
APPLICANT: Papachanasliu, Adonia E.  
APPLICANT: Green, Shawn J.  
TITLE OF INVENTION: Compositions and Methods for Inhibiting Cellular Proliferation  
TITLE OF INVENTION: Compositing TPEI Fragments  
FILE REFERENCE: 05213-0297 (43170-300210)  
CURRENT FILING DATE: 2005-07-18  
PRIORITY FILING DATE: 2001-01-22  
PRIORITY FILING DATE: 1999-01-11  
PRIORITY FILING DATE: 1997-02-06  
PRIORITY FILING DATE: 1998-08-06  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 6  
LENGTH: 213  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic peptide  
US-11-183-555-6

Query Match 91.9%; Score 1200; DB 7; Length 213;  
Best Local Similarity 100.0%; Pred. No. 1,1e-111; Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 DAAQPTGNNAICLLPLDYGPCRALLLRYYDRYQSCROPLVYGCCEGNANFYTWAC 82  
DB 1 DAAQPTGNNAICLLPLDYGPCRALLLRYYDRYQSCROPLVYGCCEGNANFYTWAC 60  
QY 83 DDAQMTIEKPKICRQVSVDDCEGSTEKYPNLSMTCEKFPSCGCHNRLENRPDB 142  
DB 61 DDAQMTIEKPKICRQVSVDDCEGSTEKYPNLSMTCEKFPSCGCHNRLENRPDB 120  
QY 143 ATCMGFCAPKIKPFCYSPKDEGLCSANVTRYFNPRTCDAFYTGCGANDNNFVSR 202  
DB 121 ATCMGFCAPKIKPFCYSPKDEGLCSANVTRYFNPRTCDAFYTGCGANDNNFVSR 180  
QY 203 DCKRACAKALKKKKKPKLRFAIRIRIRKKOP 235  
DB 181 DCKRACAKALKKKKKPKLRFAIRIRIRKKOP 213

RESULT 3  
US-10-821-234-1540  
Sequence 1540, Application US/10821234  
Publication No. US20050255114A1  
GENERAL INFORMATION:  
APPLICANT: Labat, Ivan  
APPLICANT: Stache-Crain, Birgit  
APPLICANT: Andarmani, Susan  
APPLICANT: Tang, Y. Tom  
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
FILE REFERENCE: 821A  
CURRENT APPLICATION NUMBER: US/10/821,234  
CURRENT FILING DATE: 2004-04-07  
PRIORITY FILING DATE: 2003-04-07  
PRIORITY FILING DATE: 2003-04-07  
NUMBER OF SEQ ID NOS: 1704  
SOFTWARE: pt seq\_genes Version 1.0  
SEQ ID NO 1540  
LENGTH: 304  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-821-234-1540

Query Match 29.7%; Score 388; DB 6; Length 304;  
Best Local Similarity 30.3%; Pred. No. 4.3e-31;

Matches 86; Conservative 37; Mismatches 85; Indels 76; Gaps 8;  
QY 12 LLLFTLEALGDAOE-----PTGNNAICLLPLDYGPCRALLLRYYDRYT 58  
DB 17 LLLFTLEALGDAOE-----PTGNNAICLLPLDYGPCRALLLRYYDRYT 76  
QY 59 QGCRQPLVYGCCEGNANFYTWACDACCW-----LEKVPKRLQVSDQ-- 105  
DB 77 RCEBEIYGCCEGNQGRFSLBECKKMCYRDANRILIKTTLQOEKDPFCFLB--BDPGI 133  
QY 106 CGSTEKYPNLSMTCEKFPSCGCHNRLENRPDBAICMGFC----- 149  
DB 134 CGGYITRYPNNTQKCEKFKYGGCLGNM--NNFTLBECKNICEDPENGQVNDYGTOL 191  
QY 150 -----APKTI-----PFCYSPKDEGLCSANVTRYFNPRTCDAFYTGCG 192  
DB 192 NAVNSLTPQSTKIVSLPFPHPSWCLTPADGLCRANENRTRYNSVIGKCRPKISGCG 251  
QY 193 GNDNPFVSRDECKRACAKAL-----KKKKMKLRPA 224  
DB 252 GNENFTSKQECGLRACKKGFIRISKGLIKTKRRKKQKRVKIA 295

RESULT 4  
US-11-183-555-5  
Sequence 5, Application US/1183555  
Publication No. US20060025329A1  
GENERAL INFORMATION:  
APPLICANT: Hembrough, Todd  
APPLICANT: Papachanasliu, Adonia E.  
APPLICANT: Green, Shawn J.  
TITLE OF INVENTION: Compositions and Methods for Inhibiting Cellular Proliferation  
TITLE OF INVENTION: Compositing TPEI Fragments  
FILE REFERENCE: 05213-0297 (43170-300210)  
CURRENT APPLICATION NUMBER: US/11/183,555  
CURRENT FILING DATE: 2005-07-18  
PRIORITY FILING DATE: 2001-01-22  
PRIORITY FILING DATE: 1999-01-11  
PRIORITY FILING DATE: 1999-01-11  
PRIORITY FILING DATE: 1997-02-06  
PRIORITY FILING DATE: 1998-08-06  
PRIORITY FILING DATE: 1997-02-06  
PRIORITY FILING DATE: 1998-08-06  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 5  
LENGTH: 276  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic peptide  
US-11-183-555-5

Query Match 29.4%; Score 384.5; DB 7; Length 276;  
Best Local Similarity 31.6%; Pred. No. 8.6e-31; Matches 78; Conservative 35; Mismatches 71; Indels 63; Gaps 7;

QY 36 CLPLDYGPCRALLLRYYDRYQSCROPLVYGCCEGNANFYTWACDACCW----- 88  
DB 26 CAPKADDPCKAIMRFPFNIFTRQCEBEIYGCCEGNQGRFSLBECKKMCYRDANRIL 85  
QY 89 -----LEKVPKRLQVSDQ--CEGSTEKYPNLSMTCEKFPSCGCHNRLENRPDB 142  
DB 86 KTLLOQEKDPFCFLB--EDPGICGYITRYPNNTQKCEKFKYGGCLGNM--NNFTL 140  
QY 143 ATCMGFC-----APKTI-----PFCYSPKDEGLCSA 169  
DB 141 BECKNICEDPENGQVNDYGTOLNAVNSLTPQSTKIVSLPFPHPSWCLTPADGLCSA 200  
QY 170 NTRYFNPRTCDAFYTGCGANDNNFVSRDECKRACAKAL-----KKKK 217  
DB 201 NENRTRYNSVIGKCRPKISGCGGNENFTSKQECGLRACKKGFIRISKGLIKTKRRKK 260

QY 218 MPKLRPA 224  
Db 261 KORVKIA 267

## RESULT 5

US-11-000-463-450  
Sequence 450, Application US/11000463  
Publication No. US20050266423A1  
GENERAL INFORMATION:

APPLICANT: Tang, Y Tom  
APPLICANT: Liu, Chenghua  
APPLICANT: Asundi, Vinod  
APPLICANT: Chen, Rui-hong  
APPLICANT: Qian, Xiaohong B.  
APPLICANT: Wang, Zhiwei  
APPLICANT: Wehrman, Tom  
APPLICANT: Zhou, Ping  
APPLICANT: Cao, Yi-Cheng  
APPLICANT: Dramanac, Radoje T.  
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
FILE REFERENCE: 785CIP4CN  
CURRENT APPLICATION NUMBER: US/11/000,463  
CURRENT FILING DATE: 2004-11-29  
PRIOR APPLICATION NUMBER: 10/291,265  
PRIOR FILING DATE: 2002-11-08  
PRIOR APPLICATION NUMBER: PCT/US01/02623  
PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: 09/922,279  
PRIOR FILING DATE: 2001-08-03  
PRIOR APPLICATION NUMBER: 09/491,404  
PRIOR FILING DATE: 2000-01-25  
PRIOR APPLICATION NUMBER: 09/617,746  
PRIOR FILING DATE: 2000-07-17  
PRIOR APPLICATION NUMBER: 09/631,451  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: 09/633,870  
PRIOR FILING DATE: 2000-09-15  
NUMBER OF SEQ ID NOS: 944  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 450  
LENGTH: 352  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-000-463-450

Query Match 13.8%; Score 180; DB 7; Length 352;  
Best Local Similarity 35.0%; Pred. No. 2e-10;  
Matches 42; Conservative 14; Mismatches 58; Indels 6; Gaps 3;

QY 89 IEKPVRCRLQVSVDDQCGSTGKTFYFNLSMTCKEFGGCHRRNIENRFPDEATCMGF 148  
Db 224 VTKEDSCQLGYSA-GPCMGMTSRFYNGTSMACEFYGGCGMGN--GNNFVTEKCLQT 280  
QY 149 CAPKIPSPCYSPKXGDLGSANVTRYFNPRTCTCAFTYTGCGGNDNPFVSRDDCKRAC 208  
Db 281 C---RTVAACNLPYVGPRAFIQLMAFDVAKGKCVLFPYGGCGGNGNKFYSKECREYC 337

## RESULT 6

US-11-000-463-922  
Sequence 922, Application US/11000463  
Publication No. US20050266423A1  
GENERAL INFORMATION:

APPLICANT: Tang, Y Tom  
APPLICANT: Liu, Chenghua  
APPLICANT: Asundi, Vinod  
APPLICANT: Chen, Rui-hong  
APPLICANT: Qian, Xiaohong B.  
APPLICANT: Wang, Zhiwei  
APPLICANT: Wehrman, Tom

APPLICANT: Zhang, Jie  
APPLICANT: Zhou, Ping  
APPLICANT: Cao, Yi-Cheng  
APPLICANT: Dramanac, Radoje T.  
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
FILE REFERENCE: 785CIP4CN  
CURRENT APPLICATION NUMBER: US/11/000,463  
CURRENT FILING DATE: 2004-11-29  
PRIOR APPLICATION NUMBER: 10/291,265  
PRIOR FILING DATE: 2002-11-08  
PRIOR APPLICATION NUMBER: PCT/US01/02623  
PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: 09/922,279  
PRIOR FILING DATE: 2001-08-03  
PRIOR APPLICATION NUMBER: 09/491,404  
PRIOR FILING DATE: 2000-01-25  
PRIOR APPLICATION NUMBER: 09/617,746  
PRIOR FILING DATE: 2000-07-17  
PRIOR APPLICATION NUMBER: 09/631,451  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: 09/633,870  
PRIOR FILING DATE: 2000-09-15  
NUMBER OF SEQ ID NOS: 944  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 922  
LENGTH: 352  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-000-463-922

Query Match 13.8%; Score 180; DB 7; Length 352;  
Best Local Similarity 35.0%; Pred. No. 2e-10;  
Matches 42; Conservative 14; Mismatches 58; Indels 6; Gaps 3;

QY 89 IEKPVRCRLQVSVDDQCGSTGKTFYFNLSMTCKEFGGCHRRNIENRFPDEATCMGF 148  
Db 224 VTKEDSCQLGYSA-GPCMGMTSRFYNGTSMACEFYGGCGMGN--GNNFVTEKCLQT 280  
QY 149 CAPKIPSPCYSPKXGDLGSANVTRYFNPRTCTCAFTYTGCGGNDNPFVSRDDCKRAC 208  
Db 281 C---RTVAACNLPYVGPRAFIQLMAFDVAKGKCVLFPYGGCGGNGNKFYSKECREYC 337

## RESULT 7

US-11-177-506-28  
Sequence 28, Application US/11177506  
Publication No. US20060029956A1  
GENERAL INFORMATION:

APPLICANT: Beyer, Wayne F.  
APPLICANT: Groelke, John W.  
APPLICANT: Blaesius, Rainer H.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE  
FILE REFERENCE: 46143/294851  
CURRENT APPLICATION NUMBER: US/11/177,506  
CURRENT FILING DATE: 2005-07-08  
PRIOR APPLICATION NUMBER: 60/586,856  
PRIOR FILING DATE: 2004-07-09  
NUMBER OF SEQ ID NOS: 52  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 28  
LENGTH: 352  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-177-506-28

Query Match 13.8%; Score 180; DB 7; Length 352;  
Best Local Similarity 35.0%; Pred. No. 2e-10;  
Matches 42; Conservative 14; Mismatches 58; Indels 6; Gaps 3;

QY 89 IEKPVRCRLQVSVDDQCGSTGKTFYFNLSMTCKEFGGCHRRNIENRFPDEATCMGF 148  
Db 224 VTKEDSCQLGYSA-GPCMGMTSRFYNGTSMACEFYGGCGMGN--GNNFVTEKCLQT 280  
QY 149 CAPKIPSPCYSPKXGDLGSANVTRYFNPRTCTCAFTYTGCGGNDNPFVSRDDCKRAC 208  
Db 281 C---RTVAACNLPYVGPRAFIQLMAFDVAKGKCVLFPYGGCGGNGNKFYSKECREYC 337

DB 224 VIKEDSCQGYGA-GEQMGWTSRYFYNGTSMACETFOYGCGKN--GNNFTEKELQOT 280  
QY 149 CAPKTIPSFCYSPKDEGLCSANVTRYFNPRYRTCDAFYTYGCGGNDNNFVSREDCKRAC 208  
DB 281 C---KRYAAGNLPIVKGPCAFIQWMAFDVAKKCVLPFGGCGGNGKFKYSKRECYC 337

RESULT 8  
US-11-137-465-47  
Sequence 47, Application US/11137465  
Publication No. US20050255558A1  
GENERAL INFORMATION:  
APPLICANT: Agarwal, Pankaj  
APPLICANT: Murdoch, Paul R.  
APPLICANT: Rizvi, Safia, R.  
APPLICANT: Smith, Randall, F.  
APPLICANT: Xiang, Zhaoying  
APPLICANT: Kohnick, Karen  
TITLE OF INVENTION: NOVEL COMPOUNDS  
FILE REFERENCE: GP50018  
CURRENT APPLICATION NUMBER: US/11/137,465  
PRIORITY FILING DATE: 2005-05-25  
PRIORITY APPLICATION NUMBER: US/10/239,663  
PRIORITY FILING DATE: 2002-09-24  
PRIORITY APPLICATION NUMBER: PCT/US01/09226  
PRIORITY FILING DATE: 2001-03-22  
PRIORITY APPLICATION NUMBER: 60/192,158  
PRIORITY FILING DATE: 2000-03-24  
PRIORITY APPLICATION NUMBER: 60/192,668  
PRIORITY FILING DATE: 2000-03-27  
PRIORITY APPLICATION NUMBER: 60/200,166  
PRIORITY FILING DATE: 2000-04-27  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 47  
LENGTH: 548  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-137-465-47

Query Match 13.7%; Score 179.5; DB 7; Length 548;  
Best Local Similarity 32.8%; Pred. No. 3.6e-10;  
Matches 45; Conservative 21; Mismatches 64; Indels 7; Gaps 3;

QY 18 EALGDAOEPTGNNAEICLLPDYGGPCRALLRYYDRYTGSCROQFLYGGCGGNANFY 77  
DB 345 EACQACARBP---GDACVLPAYGSPCRGMEPRMAYSPLOQCHFPYVGGCGGNANFY 400  
QY 78 TWACDADACWRIKVP--KYCRLQVSVDDQCEGSTEREFNLSSMTCEKFPSSGCHRNRI 135  
DB 401 SRSCEBDAC-PVPRTPPCRCRLRSKLALSLCRSDFAIVGRLTEVLEPEPAAGIARVAL 459  
QY 136 ENRFPDEATCMGFCAPK 152  
DB 460 EDVLKDDKMKGLKFLGTK 476

RESULT 9  
US-10-821-234-1123  
Sequence 1123, Application US/10821234  
Publication No. US20050255114A1  
GENERAL INFORMATION:  
APPLICANT: Labat, Ivan  
APPLICANT: Stache-Crahn, Birgit  
APPLICANT: Andarmani, Susan  
APPLICANT: Tang, Y. Tom  
TITLE OF INVENTION: Methods for diagnosis and treatment of Preeclampsia  
FILE REFERENCE: 821A  
CURRENT APPLICATION NUMBER: US/10/821,234  
PRIORITY FILING DATE: 2004-04-07  
PRIORITY APPLICATION NUMBER: US 60/462,047  
PRIORITY FILING DATE: 2003-04-07  
NUMBER OF SEQ ID NOS: 1704

SOFTWARE: pt\_SEQ\_genes Version 1.0  
SEQ ID NO 1123  
LENGTH: 94  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-821-234-1123

Query Match 12.3%; Score 160; DB 6; Length 94;  
Best Local Similarity 43.9%; Pred. No. 5e-09;  
Matches 25; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

QY 158 CYSPKDEGLCSANVTRYFNPRYRTCDAFYTYGCGGNDNNFVSREDCKRACAKALX 214  
DB 29 CXLPKDEGTGRDPIFKMYDPTKSCARFWYGGCGGNGENKFGSQKCEHYCAPLVLA 85

RESULT 10  
US-11-068-783-54  
Sequence 54, Application US/11068783  
Publication No. US20050260715A1  
GENERAL INFORMATION:  
APPLICANT: Burian, Jan  
APPLICANT: Bartfeld, Daniel  
TITLE OF INVENTION: EFFICIENT METHODS FOR PRODUCING  
TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES IN HOST CELLS  
FILE REFERENCE: 660081.411  
CURRENT APPLICATION NUMBER: US/11/068,783  
PRIORITY FILING DATE: 2005-02-28  
PRIORITY APPLICATION NUMBER: US/09/444,281  
PRIORITY FILING DATE: 1999-11-19  
NUMBER OF SEQ ID NOS: 113  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 54  
LENGTH: 58  
TYPE: PRT  
ORGANISM: Bos taurus  
US-11-068-783-54

Query Match 11.2%; Score 146; DB 7; Length 58;  
Best Local Similarity 43.9%; Pred. No. 7.5e-08;  
Matches 25; Conservative 4; Mismatches 28; Indels 0; Gaps 0;

QY 155 PSFCYSPKDEGLCSANVTRYFNPRYRTCDAFYTYGCGGNDNNFVSREDCKRACAKA 211  
DB 2 PFCLEPFTYGTGRKRIIRYFNAYAGLQGTFTVYGGCGCRKRNNFSAEDCMRTCGA 58

RESULT 11  
US-10-982-545-15  
Sequence 15, Application US/10982545  
Publication No. US20050244890A1  
GENERAL INFORMATION:  
APPLICANT: Davies, Huw Alun  
APPLICANT: McGuire, James  
APPLICANT: Simonson, Anja Hvild  
APPLICANT: Blennow, Kaj  
APPLICANT: Podust, Vladimir  
APPLICANT: Ciplergen Biosystems, Inc.  
TITLE OF INVENTION: Biomarkers for Alzheimer's Disease  
FILE REFERENCE: 016866-011550US  
CURRENT APPLICATION NUMBER: US/10/982,545  
PRIORITY FILING DATE: 2004-11-06  
PRIORITY APPLICATION NUMBER: US 60/518,360  
PRIORITY FILING DATE: 2003-11-07  
PRIORITY APPLICATION NUMBER: US 60/526,753  
PRIORITY FILING DATE: 2003-12-02  
PRIORITY APPLICATION NUMBER: US 60/546,423  
PRIORITY FILING DATE: 2004-02-19  
PRIORITY APPLICATION NUMBER: US 60/547,250  
PRIORITY FILING DATE: 2004-02-23  
PRIORITY APPLICATION NUMBER: US 60/558,896  
PRIORITY FILING DATE: 2004-04-02  
PRIORITY APPLICATION NUMBER: US 60/572,617

PRIOR FILING DATE: 2004-05-18  
PRIOR APPLICATION NUMBER: US 60/586,503  
PRIOR FILING DATE: 2004-07-08  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 770  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Amyloid beta A4 precursor (APP, ABPP), isoform a, protease  
OTHER INFORMATION: nexin II (PN-II), cerebral vascular amyloid peptide (CVAP),  
OTHER INFORMATION: amyloid-beta protein, beta-amyloid peptide, A4 amyloid protein,  
OTHER INFORMATION: Alzheimer's disease amyloid protein  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: (1)..(17)  
OTHER INFORMATION: signal peptide  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(40)  
OTHER INFORMATION: biomarker peptide 4320 Da (IMC-NI), A-beta 1-40  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (18)..(671)  
OTHER INFORMATION: soluble APP-alpha  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (672)..(770)  
OTHER INFORMATION: C99  
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NAME/KEY: PEPTIDE  
LOCATION: (672)..(713)  
OTHER INFORMATION: beta-amyloid protein 42  
FEATURE:  
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LOCATION: (672)..(711)  
OTHER INFORMATION: biomarker peptide 4330 Da, fragment of Amyloid  
OTHER INFORMATION: beta A4 precursor, beta-amyloid protein 40  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (688)..(770)  
OTHER INFORMATION: C83  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (688)..(713)  
OTHER INFORMATION: P3(42)  
FEATURE:  
NAME/KEY: PEPTIDE  
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OTHER INFORMATION: P3(40)  
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NAME/KEY: PEPTIDE  
LOCATION: (712)..(770)  
OTHER INFORMATION: gamma-CTF(59)  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (714)..(770)  
OTHER INFORMATION: gamma-CTF(57)  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (721)..(770)  
OTHER INFORMATION: gamma-CTF(50)  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (740)..(770)  
OTHER INFORMATION: C31  
US-10-982-545-15

Query Match 10.8%; Score 141; DB 6; Length 770;  
Best Local Similarity 47.2%; Pred. No. 3.3e-06;  
Matches 25; Conservative 6; Mismatches 22; Indels 0; Gaps 0;  
Db 289 EVCSBQAFGPGCRAMISRWFYDVBGKCAPFFYGGGGRNNRNDTEYCAVC 341  
34 EICLPLDYGPCGALLARYYDRYTSQCRQFLYGGCGGNANFYTWACDDAC 86  
US-10-789-273-38  
Sequence 38, Application US/10789273  
Publication No. US20050249725A1  
GENERAL INFORMATION:  
APPLICANT: Basi, Gurig  
APPLICANT: Saldanha, Jose  
APPLICANT: Yednock, Ted  
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
TITLE OF INVENTION: BETA-AMYLOID PEPTIDE  
FILE REFERENCE: ELN-002CP  
CURRENT APPLICATION NUMBER: US/10/789,273  
CURRENT FILING DATE: 2004-02-27  
PRIOR APPLICATION NUMBER: US/10/388,389  
PRIOR FILING DATE: 2003-03-12  
PRIOR APPLICATION NUMBER: US 10/010,942  
PRIOR FILING DATE: 2001-12-06  
PRIOR APPLICATION NUMBER: US 60/251,892  
PRIOR FILING DATE: 2000-12-06  
NUMBER OF SEQ ID NOS: 63  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 38  
LENGTH: 770  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-789-273-38  
Query Match 10.8%; Score 141; DB 6; Length 770;  
Best Local Similarity 47.2%; Pred. No. 3.3e-06;  
Matches 25; Conservative 6; Mismatches 22; Indels 0; Gaps 0;  
Db 289 EVCSBQAFGPGCRAMISRWFYDVBGKCAPFFYGGGGRNNRNDTEYCAVC 341  
34 EICLPLDYGPCGALLARYYDRYTSQCRQFLYGGCGGNANFYTWACDDAC 86  
US-10-821-234-1619  
Sequence 1619, Application US/10821234  
Publication No. US20050255114A1  
GENERAL INFORMATION:  
APPLICANT: Labat, Ivan  
APPLICANT: Stache-Crain, Birgit  
APPLICANT: Andarmant, Susan  
APPLICANT: Tang, Y. Tom  
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
FILE REFERENCE: 821A  
CURRENT APPLICATION NUMBER: US/10/821,234  
CURRENT FILING DATE: 2004-04-07  
PRIOR APPLICATION NUMBER: US 60/462,047  
PRIOR FILING DATE: 2003-04-07  
NUMBER OF SEQ ID NOS: 1704  
SOFTWARE: PC\_SEQ\_genes Version 1.0  
SEQ ID NO 1619  
LENGTH: 763  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-821-234-1619  
Query Match 10.0%; Score 130; DB 6; Length 763;  
Best Local Similarity 28.6%; Pred. No. 4e-05;  
Matches 34; Conservative 17; Mismatches 48; Indels 20; Gaps 3;



GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 9, 2006, 19:57:44 ; Search time 566 Seconds

(without alignments)  
573.780 Million cell updates/sec

Title: US-10-800-057-2

Perfect score: 1306

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Gapop 10.0 , Gapext 0.5

Searched: 7861189 seqs, 1381955077 residues

Total number of hits satisfying chosen parameters: 7861189

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA Main:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1306	100.0	235	1	PCT-US02-04915-52
3	1306	100.0	235	1	PCT-US02-07826-316
4	1306	100.0	235	1	PCT-US02-34777-332
5	1306	100.0	235	1	PCT-US94-12609-2
6	1306	100.0	235	18	US-08-800-483-4
7	1306	100.0	235	22	US-09-265-627-2
8	1306	100.0	235	23	US-09-308-853-4
9	1306	100.0	235	24	US-09-466-867-332
10	1306	100.0	235	24	US-09-476-300-332
11	1306	100.0	235	25	US-09-533-077-332
12	1306	100.0	235	25	US-09-546-229-332
13	1306	100.0	235	25	US-09-560-406-332
14	1306	100.0	235	26	US-09-677-419A-332
15	1306	100.0	235	27	US-09-760-443-1224
16	1306	100.0	235	27	US-09-760-447-41
17	1306	100.0	235	27	US-09-784-356-119
18	1306	100.0	235	27	US-09-791-537-96446
19	1306	100.0	235	28	US-09-849-626-332
20	1306	100.0	235	29	US-09-902-941-332
21	1306	100.0	235	30	US-10-021-660-119
22	1306	100.0	235	30	US-10-060-036-167
23	1306	100.0	235	30	US-10-097-340-316
24	1306	100.0	235	31	US-10-113-872-332
25	1306	100.0	235	31	US-10-126-052A-397
26	1306	100.0	235	31	US-10-130-138B-202
27	1306	100.0	235	31	US-10-137-441-41
28	1306	100.0	235	31	US-10-170-205B-764
29	1306	100.0	235	32	US-10-211-462-52
30	1306	100.0	235	32	US-10-212-054-1224
31	1306	100.0	235	32	US-10-283-017-332
32	1306	100.0	235	32	US-10-295-027-24
33	1306	100.0	235	34	US-10-405-027-3268
34	1306	100.0	235	34	US-10-428-467-7
35	1306	100.0	235	36	US-10-680-684-2
36	1306	100.0	235	38	US-10-800-057-2
37	1306	100.0	235	38	US-10-821-234-1398
38	1306	100.0	235	38	US-10-821-861-886
39	1306	100.0	235	39	US-10-940-774-6735
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41	1306	100.0	235	39	US-10-991-321-24
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43	1306	100.0	235	48	US-60-406-385-190
44	1306	100.0	235	48	US-60-453-050-11171
45	1306	100.0	235	48	US-60-453-135-11171

#### ALIGNMENTS

RESULT 1  
PCT-US02-02781-167  
; Sequence 167, Application PC/TUS0202781  
; GENERAL INFORMATION:  
; APPLICANT: Corixa Corporation

APPLICANT: Benson, Darin R.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Lodes, Michael J.  
APPLICANT: Persing, David H.  
APPLICANT: Hepler, William T.  
APPLICANT: Jiang, Yugu  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.566PC  
CURRENT APPLICATION NUMBER: PCT/US02/02781  
CURRENT FILING DATE: 2002-01-30  
NUMBER OF SEQ ID NOS: 4560  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 167  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Homo sapiens  
PCT-US02-02781-167

Query Match 100.0%; Score 1306; DB 1; Length 235;  
Best Local Similarity 100.0%; Pred. No. 7.7e-138;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 TCEKFFSGGCHNRRIENRPDEATCMGFCAPKKIPSCYSPDQGLCSANVTRYENPRY 180  
QY 181 RTCDATFTYTGCGGNDNNFVSRDCKRACAKALKKKKKMPKJLPFASIRIRIKRKQF 235  
DB 181 RTCDATFTYTGCGGNDNNFVSRDCKRACAKALKKKKKMPKJLPFASIRIRIKRKQF 235

RESULT 2  
PCT-US02-04915-52  
Sequence 52, Application PC/TUS0204915  
GENERAL INFORMATION:  
APPLICANT: Murray, Richard  
APPLICANT: Glynn, Richard  
APPLICANT: Watson, Susan R.  
APPLICANT: Aziz, Natsaba  
APPLICANT: Eos Biotechnology, Inc.  
TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and  
FILE REFERENCE: 018501-006200PC  
CURRENT APPLICATION NUMBER: PCT/US02/04915  
CURRENT FILING DATE: 2002-02-14  
PRIOR APPLICATION NUMBER: US 09/784,356  
PRIOR FILING DATE: 2001-02-14  
PRIOR APPLICATION NUMBER: US 09/791,390  
PRIOR FILING DATE: 2001-02-22  
PRIOR APPLICATION NUMBER: US 60/285,475  
PRIOR FILING DATE: 2002-04-19  
PRIOR APPLICATION NUMBER: US 60/310,025  
PRIOR FILING DATE: 2001-08-03  
PRIOR APPLICATION NUMBER: US 60/350,666  
PRIOR FILING DATE: 2001-11-13  
PRIOR APPLICATION NUMBER: US 60/334,244  
PRIOR FILING DATE: 2001-11-29  
NUMBER OF SEQ ID NOS: 230  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 52  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Homo sapiens  
PCT-US02-04915-52

Query Match 100.0%; Score 1306; DB 1; Length 235;  
Best Local Similarity 100.0%; Pred. No. 7.7e-138;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MDPARPLGISILLFLTEALGDAAPPTGNNAEICLLPLDYGPCRALLRYYDRYTOS 60  
QY 61 CRQFLYGGCEGNANFYTWACDCAWRIEKVPKVCRLQVSDVDOCEGSTEKFFNLSM 120  
DB 61 CRQFLYGGCEGNANFYTWACDCAWRIEKVPKVCRLQVSDVDOCEGSTEKFFNLSM 120  
QY 121 TCEKFFSGGCHNRRIENRPDEATCMGFCAPKKIPSCYSPDQGLCSANVTRYENPRY 180  
DB 121 TCEKFFSGGCHNRRIENRPDEATCMGFCAPKKIPSCYSPDQGLCSANVTRYENPRY 180  
QY 181 RTCDATFTYTGCGGNDNNFVSRDCKRACAKALKKKKKMPKJLPFASIRIRIKRKQF 235  
DB 181 RTCDATFTYTGCGGNDNNFVSRDCKRACAKALKKKKKMPKJLPFASIRIRIKRKQF 235

RESULT 3  
PCT-US02-07826-316  
Sequence 316, Application PC/TUS0207826  
GENERAL INFORMATION:  
APPLICANT: Millennium Pharmaceuticals, Inc. et al.  
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,  
FILE REFERENCE: MRI-030PC  
CURRENT APPLICATION NUMBER: PCT/US02/07826  
CURRENT FILING DATE: 2002-03-14  
PRIOR APPLICATION NUMBER: 60/276,025  
PRIOR FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 60/325,149  
PRIOR FILING DATE: 2001-09-27  
PRIOR APPLICATION NUMBER: 60/276,026  
PRIOR FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 60/324,967  
PRIOR FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: 60/311,732  
PRIOR FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: 60/325,102  
PRIOR FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: 60/323,580  
PRIOR FILING DATE: 2001-09-19  
NUMBER OF SEQ ID NOS: 363  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 316  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Homo sapiens  
PCT-US02-07826-316

Query Match 100.0%; Score 1306; DB 1; Length 235;  
Best Local Similarity 100.0%; Pred. No. 7.7e-138;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGISILLFLTEALGDAAPPTGNNAEICLLPLDYGPCRALLRYYDRYTOS 60  
DB 1 MDPARPLGISILLFLTEALGDAAPPTGNNAEICLLPLDYGPCRALLRYYDRYTOS 60  
QY 61 CRQFLYGGCEGNANFYTWACDCAWRIEKVPKVCRLQVSDVDOCEGSTEKFFNLSM 120  
DB 61 CRQFLYGGCEGNANFYTWACDCAWRIEKVPKVCRLQVSDVDOCEGSTEKFFNLSM 120  
QY 121 TCEKFFSGGCHNRRIENRPDEATCMGFCAPKKIPSCYSPDQGLCSANVTRYENPRY 180  
DB 121 TCEKFFSGGCHNRRIENRPDEATCMGFCAPKKIPSCYSPDQGLCSANVTRYENPRY 180  
QY 181 RTCDATFTYTGCGGNDNNFVSRDCKRACAKALKKKKKMPKJLPFASIRIRIKRKQF 235  
DB 181 RTCDATFTYTGCGGNDNNFVSRDCKRACAKALKKKKKMPKJLPFASIRIRIKRKQF 235



RESULT 4  
PCT-US02-34777-332  
Sequence 332, Application PC/TUS0234777  
GENERAL INFORMATION:  
APPLICANT: Corixa Corporation  
APPLICANT: Henderson, Robert A.  
APPLICANT: Wang, Tonglong  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Kalos, Michael D.  
APPLICANT: Sleath, Paul R.  
APPLICANT: Johnson, Jeffrey C.  
APPLICANT: Retter, Marc W.  
APPLICANT: Durham, Margarita  
APPLICANT: Carter, Darick  
APPLICANT: Panger, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: McNabb, Andria  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.47803PC  
CURRENT APPLICATION NUMBER: PCT/US02/34777  
CURRENT FILING DATE: 2002-10-28  
NUMBER OF SEQ ID NOS: 2157  
SOFTWARE: PaeSSE0 for Windows Version 4.0  
SEQ ID NO 332  
LENGTH: 235  
TYPE: PRP  
ORGANISM: Homo sapiens  
PCT-US02-34777-332

Query Match 100.0%; Score 1306; DB 1; Length 235;  
Best Local Similarity 100.0%; Pred. No. 7,7e-138;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAPPLGSLILLPLTEALGDAAQEPYNNACILPLDYGPCRALILRYTYRYS 60  
DB 1 MDPAPPLGSLILLPLTEALGDAAQEPYNNACILPLDYGPCRALILRYTYRYS 60  
QY 61 CRQFLYGGCEGNANFYTWACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKTFNLSM 120  
DB 61 CRQFLYGGCEGNANFYTWACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKTFNLSM 120  
QY 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKKIPSCYSPDQELCSANTRYTFNRY 180  
DB 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKKIPSCYSPDQELCSANTRYTFNRY 180  
QY 181 RTCDAFYTYGGGNDNNFVSRDCKRACAKALKKKKKMPKLRFAIRIRIRKKQF 235  
DB 181 RTCDAFYTYGGGNDNNFVSRDCKRACAKALKKKKKMPKLRFAIRIRIRKKQF 235

RESULT 5  
PCT-US94-12609-2  
Sequence 2, Application PC/TUS9412609  
GENERAL INFORMATION:  
APPLICANT: ZymoGenetics, Inc.  
APPLICANT: 1201 Baseline Avenue East  
APPLICANT: Seattle  
APPLICANT: WA  
APPLICANT: US  
APPLICANT: 98102  
APPLICANT: Scholles Hall 102  
APPLICANT: Albuquerque  
APPLICANT: NM  
APPLICANT: US  
APPLICANT: 87131  
TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS AND  
TITLE OF INVENTION: METHODS RELATING THERETO  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:

ADDRESSEE: ZymoGenetics, Inc.  
STREET: 1201 Baseline Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/12609  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, Gary B  
REGISTRATION NUMBER: 31-648  
REFERENCE/DOCKET NUMBER: 93-14PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6673  
TELEFAX: 206-442-6678  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US94-12609-2

Query Match 100.0%; Score 1306; DB 1; Length 235;  
Best Local Similarity 100.0%; Pred. No. 7,7e-138;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAPPLGSLILLPLTEALGDAAQEPYNNACILPLDYGPCRALILRYTYRYS 60  
DB 1 MDPAPPLGSLILLPLTEALGDAAQEPYNNACILPLDYGPCRALILRYTYRYS 60  
QY 61 CRQFLYGGCEGNANFYTWACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKTFNLSM 120  
DB 61 CRQFLYGGCEGNANFYTWACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKTFNLSM 120  
QY 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKKIPSCYSPDQELCSANTRYTFNRY 180  
DB 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKKIPSCYSPDQELCSANTRYTFNRY 180  
QY 181 RTCDAFYTYGGGNDNNFVSRDCKRACAKALKKKKKMPKLRFAIRIRIRKKQF 235  
DB 181 RTCDAFYTYGGGNDNNFVSRDCKRACAKALKKKKKMPKLRFAIRIRIRKKQF 235

RESULT 6  
US-08-800-483-4  
Sequence 4, Application US/08800483  
GENERAL INFORMATION:  
APPLICANT: Rao, Chilkuri N.  
APPLICANT: Woodley, David T.  
TITLE OF INVENTION: USES OF SERINE PROTEASE INHIBITORS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheridan Rose P. C.  
STREET: 1700 Lincoln Street, Suite 3500  
CITY: Denver  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/800,483



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QY 1 MDPARPLGISILLFLTEBALGDAOEPYGNNAEICLLPLDYGPCRALILRYYYDRYTOS 60
DB 1 MDPARPLGISILLFLTEBALGDAOEPYGNNAEICLLPLDYGPCRALILRYYYDRYTOS 60
QY 61 CROPLYGCGEGNANNFYTWACDCAWRIEKVPKVCRLQVSVDDQCEGSTEKYPFNLSSM 120
DB 61 CROPLYGCGEGNANNFYTWACDCAWRIEKVPKVCRLQVSVDDQCEGSTEKYPFNLSSM 120
QY 121 TCEKFFSGGCHNRRLENRPDEATCMGFCAPKKIISFCYSPDQEGLCSANVTTRYFNPRY 180
DB 121 TCEKFFSGGCHNRRLENRPDEATCMGFCAPKKIISFCYSPDQEGLCSANVTTRYFNPRY 180
QY 181 RTCDAFYTYGCGGNDNNFVSRBDCRCAKAKLKKKKMPKLPASRIRIKRKQF 235
DB 181 RTCDAFYTYGCGGNDNNFVSRBDCRCAKAKLKKKKMPKLPASRIRIKRKQF 235

RESULT 10
US-09-476-300-332
; Sequence 332, Application US/09476300
; GENERAL INFORMATION:
; APPLICANT: Bangur, Tongtong
; APPLICANT: Bangur, Chaltanya S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C3
; CURRENT APPLICATION NUMBER: US/09/476,300
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 785
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-476-300-332

Query Match 100.0%; Score 1306; DB 24; Length 235;
Best Local Similarity 100.0%; Pred. No. 7.7e-138;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGISILLFLTEBALGDAOEPYGNNAEICLLPLDYGPCRALILRYYYDRYTOS 60
DB 1 MDPARPLGISILLFLTEBALGDAOEPYGNNAEICLLPLDYGPCRALILRYYYDRYTOS 60
QY 61 CROPLYGCGEGNANNFYTWACDCAWRIEKVPKVCRLQVSVDDQCEGSTEKYPFNLSSM 120
DB 61 CROPLYGCGEGNANNFYTWACDCAWRIEKVPKVCRLQVSVDDQCEGSTEKYPFNLSSM 120
QY 121 TCEKFFSGGCHNRRLENRPDEATCMGFCAPKKIISFCYSPDQEGLCSANVTTRYFNPRY 180
DB 121 TCEKFFSGGCHNRRLENRPDEATCMGFCAPKKIISFCYSPDQEGLCSANVTTRYFNPRY 180
QY 181 RTCDAFYTYGCGGNDNNFVSRBDCRCAKAKLKKKKMPKLPASRIRIKRKQF 235
DB 181 RTCDAFYTYGCGGNDNNFVSRBDCRCAKAKLKKKKMPKLPASRIRIKRKQF 235

RESULT 11
US-09-533-077-332
; Sequence 332, Application US/09533077
; GENERAL INFORMATION:
; APPLICANT: Bangur, Tongtong
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C5
; CURRENT APPLICATION NUMBER: US/09/533,077
; CURRENT FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 800
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 332
```

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; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-533-077-332

Query Match 100.0%; Score 1306; DB 25; Length 235;
Best Local Similarity 100.0%; Pred. No. 7.7e-138;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGISILLFLTEBALGDAOEPYGNNAEICLLPLDYGPCRALILRYYYDRYTOS 60
DB 1 MDPARPLGISILLFLTEBALGDAOEPYGNNAEICLLPLDYGPCRALILRYYYDRYTOS 60
QY 61 CROPLYGCGEGNANNFYTWACDCAWRIEKVPKVCRLQVSVDDQCEGSTEKYPFNLSSM 120
DB 61 CROPLYGCGEGNANNFYTWACDCAWRIEKVPKVCRLQVSVDDQCEGSTEKYPFNLSSM 120
QY 121 TCEKFFSGGCHNRRLENRPDEATCMGFCAPKKIISFCYSPDQEGLCSANVTTRYFNPRY 180
DB 121 TCEKFFSGGCHNRRLENRPDEATCMGFCAPKKIISFCYSPDQEGLCSANVTTRYFNPRY 180
QY 181 RTCDAFYTYGCGGNDNNFVSRBDCRCAKAKLKKKKMPKLPASRIRIKRKQF 235
DB 181 RTCDAFYTYGCGGNDNNFVSRBDCRCAKAKLKKKKMPKLPASRIRIKRKQF 235

RESULT 12
US-09-546-259-332
; Sequence 332, Application US/09546259
; GENERAL INFORMATION:
; APPLICANT: Bangur, Tongtong
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Manion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C6
; CURRENT APPLICATION NUMBER: US/09/546,259
; CURRENT FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 803
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-546-259-332

Query Match 100.0%; Score 1306; DB 25; Length 235;
Best Local Similarity 100.0%; Pred. No. 7.7e-138;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGISILLFLTEBALGDAOEPYGNNAEICLLPLDYGPCRALILRYYYDRYTOS 60
DB 1 MDPARPLGISILLFLTEBALGDAOEPYGNNAEICLLPLDYGPCRALILRYYYDRYTOS 60
QY 61 CROPLYGCGEGNANNFYTWACDCAWRIEKVPKVCRLQVSVDDQCEGSTEKYPFNLSSM 120
DB 61 CROPLYGCGEGNANNFYTWACDCAWRIEKVPKVCRLQVSVDDQCEGSTEKYPFNLSSM 120
QY 121 TCEKFFSGGCHNRRLENRPDEATCMGFCAPKKIISFCYSPDQEGLCSANVTTRYFNPRY 180
DB 121 TCEKFFSGGCHNRRLENRPDEATCMGFCAPKKIISFCYSPDQEGLCSANVTTRYFNPRY 180
QY 181 RTCDAFYTYGCGGNDNNFVSRBDCRCAKAKLKKKKMPKLPASRIRIKRKQF 235
DB 181 RTCDAFYTYGCGGNDNNFVSRBDCRCAKAKLKKKKMPKLPASRIRIKRKQF 235

RESULT 13
US-09-560-406-332
; Sequence 332, Application US/09560406
; GENERAL INFORMATION:
; APPLICANT: Bangur, Tongtong
```

```
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: Lodes, Michael A.
/ APPLICANT: Ranger, Gary
/ APPLICANT: Vedvick, Tom
/ APPLICANT: Carter, Darlick
/ APPLICANT: Retter, Marc
/ APPLICANT: Mannion, Jane
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
/ FILE REFERENCE: 210121.478C7
/ CURRENT APPLICATION NUMBER: US/09/560,406
/ CURRENT FILING DATE: 2000-04-27
/ NUMBER OF SEQ ID NOS: 824
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 332
/ LENGTH: 235
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-560-406-332
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Query Match      100.0%; Score 1306; DB 25; Length 235;
Best Local Similarity 100.0%; Pred. No. 7,7e-138;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MDPARPLGSLILLFLTEALGDAAQEPYNNABICLLPLDYGPCRALLLRYYDRYTOS 60
DB 1 MDPARPLGSLILLFLTEALGDAAQEPYNNABICLLPLDYGPCRALLLRYYDRYTOS 60
QY 61 CRQFLYGGCEGNANFYTWBACDDACMRIBKYPKVCRLQVSDVDDCGESTTEKFFNLSSM 120
DB 61 CRQFLYGGCEGNANFYTWBACDDACMRIBKYPKVCRLQVSDVDDCGESTTEKFFNLSSM 120
QY 121 TCEKFFSGGCHNRIRNRPDEATCMGFCAPKIPSCYSPDDEGLCSANVTRYFNPRY 180
DB 121 TCEKFFSGGCHNRIRNRPDEATCMGFCAPKIPSCYSPDDEGLCSANVTRYFNPRY 180
QY 181 RTCDAFYTYGCGNDNPFVSRBDCKRACAKALKKKKKMPKLRPASIRIRIKRKQP 235
DB 181 RTCDAFYTYGCGNDNPFVSRBDCKRACAKALKKKKKMPKLRPASIRIRIKRKQP 235
```

```
RESULT 14
US-09-677-419A-332
/ Sequence 332, Application US/09677419A
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Tonglong
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: Lodes, Michael J.
/ APPLICANT: Ranger, Gary R.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Darlick
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Mannion, Jane
/ APPLICANT: Fan, Liqun
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE REFERENCE: 210121.478C13
/ CURRENT APPLICATION NUMBER: US/09/677,419A
/ CURRENT FILING DATE: 2000-10-06
/ NUMBER OF SEQ ID NOS: 1825
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 332
/ LENGTH: 235
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-677-419A-332
```

```
Query Match      100.0%; Score 1306; DB 26; Length 235;
Best Local Similarity 100.0%; Pred. No. 7,7e-138;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 MDPARPLGSLILLFLTEALGDAAQEPYNNABICLLPLDYGPCRALLLRYYDRYTOS 60
DB 1 MDPARPLGSLILLFLTEALGDAAQEPYNNABICLLPLDYGPCRALLLRYYDRYTOS 60
```

```
DB 1 MDPARPLGSLILLFLTEALGDAAQEPYNNABICLLPLDYGPCRALLLRYYDRYTOS 60
QY 61 CRQFLYGGCEGNANFYTWBACDDACMRIBKYPKVCRLQVSDVDDCGESTTEKFFNLSSM 120
DB 61 CRQFLYGGCEGNANFYTWBACDDACMRIBKYPKVCRLQVSDVDDCGESTTEKFFNLSSM 120
QY 121 TCEKFFSGGCHNRIRNRPDEATCMGFCAPKIPSCYSPDDEGLCSANVTRYFNPRY 180
DB 121 TCEKFFSGGCHNRIRNRPDEATCMGFCAPKIPSCYSPDDEGLCSANVTRYFNPRY 180
QY 181 RTCDAFYTYGCGNDNPFVSRBDCKRACAKALKKKKKMPKLRPASIRIRIKRKQP 235
DB 181 RTCDAFYTYGCGNDNPFVSRBDCKRACAKALKKKKKMPKLRPASIRIRIKRKQP 235
```

```
RESULT 15
US-09-760-443-1224
/ Sequence 1224, Application US/09760443
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
/ FILE REFERENCE: PZJ12
/ CURRENT APPLICATION NUMBER: US/09/760,443
/ Prior application data removed - refer to PALM or file wrapper
/ NUMBER OF SEQ ID NOS: 2164
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1224
/ LENGTH: 235
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-760-443-1224
```

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Query Match      100.0%; Score 1306; DB 27; Length 235;
Best Local Similarity 100.0%; Pred. No. 7,7e-138;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 MDPARPLGSLILLFLTEALGDAAQEPYNNABICLLPLDYGPCRALLLRYYDRYTOS 60
DB 1 MDPARPLGSLILLFLTEALGDAAQEPYNNABICLLPLDYGPCRALLLRYYDRYTOS 60
QY 61 CRQFLYGGCEGNANFYTWBACDDACMRIBKYPKVCRLQVSDVDDCGESTTEKFFNLSSM 120
DB 61 CRQFLYGGCEGNANFYTWBACDDACMRIBKYPKVCRLQVSDVDDCGESTTEKFFNLSSM 120
QY 121 TCEKFFSGGCHNRIRNRPDEATCMGFCAPKIPSCYSPDDEGLCSANVTRYFNPRY 180
DB 121 TCEKFFSGGCHNRIRNRPDEATCMGFCAPKIPSCYSPDDEGLCSANVTRYFNPRY 180
QY 181 RTCDAFYTYGCGNDNPFVSRBDCKRACAKALKKKKKMPKLRPASIRIRIKRKQP 235
DB 181 RTCDAFYTYGCGNDNPFVSRBDCKRACAKALKKKKKMPKLRPASIRIRIKRKQP 235
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Search completed: March 9, 2006, 20:07:58
Job time : 568 secs
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 9, 2006, 19:58:39 ; Search time 39 seconds

(without alignments)  
478.910 Million cell updates/sec

Title: US-10-800-057-2

Perfect score: 1306

Sequence: 1 MDPAPPLGSLILFLTEA.....KMPKLRPASRIKRIKQF 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 339805 seqs, 79478670 residues

Total number of hits satisfying chosen parameters: 339805

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New:\*  
1: /cgn2\_6/prodata/1/paa/PCT\_NEW\_COMB.pep.\*  
2: /cgn2\_6/prodata/1/paa/US06\_NEW\_COMB.pep.\*  
3: /cgn2\_6/prodata/1/paa/US07\_NEW\_COMB.pep.\*  
4: /cgn2\_6/prodata/1/paa/US08\_NEW\_COMB.pep.\*  
5: /cgn2\_6/prodata/1/paa/US09\_NEW\_COMB.pep.\*  
6: /cgn2\_6/prodata/1/paa/US10\_NEW\_COMB.pep.\*  
7: /cgn2\_6/prodata/1/paa/US11\_NEW\_COMB.pep.\*  
8: /cgn2\_6/prodata/1/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1306	100.0	235	7	US-11-301-554-332
2	1200	91.9	213	7	US-11-107-643-1
3	421	32.2	73	7	US-11-107-643-2
4	418	32.0	73	7	US-11-107-643-3
5	388	29.7	304	1	PCT-US05-42298-1
6	388	29.7	304	1	PCT-US05-34335-54
7	388	29.7	304	7	US-11-287-121A-1
8	384.5	29.4	276	7	US-11-302-208-1
9	384.5	29.4	276	7	US-11-337-518-1
10	343	26.3	58	1	PCT-US05-42298-4
11	343	26.3	58	1	PCT-US05-34335-37
12	343	26.3	58	7	US-11-287-121A-4
13	342	26.2	61	1	PCT-US05-42298-16
14	342	26.2	61	1	PCT-US05-34335-38
15	342	26.2	61	7	US-11-287-121A-16
16	334	25.6	58	1	PCT-US05-34335-39
17	320	24.5	56	1	PCT-US05-42298-11
18	312	23.9	56	7	US-11-287-121A-11
19	312	23.9	56	7	US-11-287-121A-11
20	305	23.4	68	8	US-60-763-373-177
21	305	23.4	1487	8	US-60-772-265-1
22	265	20.3	513	7	US-11-268-554-187
23	265	20.3	513	8	US-60-735-818-3
24	265	20.3	513	8	US-60-741-050-21
25	265	20.3	513	8	US-60-763-365-24

26	265	20.3	513	8	US-60-763-365-26	Sequence 26, App1
27	265	20.3	513	8	US-60-763-374-86	Sequence 86, App1
28	262	20.1	529	7	US-11-268-554-188	Sequence 188, App1
29	262	20.1	529	8	US-60-735-818-1	Sequence 1, App1
30	262	20.1	529	8	US-60-735-818-2	Sequence 2, App1
31	262	20.1	529	8	US-60-763-365-25	Sequence 25, App1
32	262	20.1	529	8	US-60-763-365-27	Sequence 27, App1
33	262	20.1	529	8	US-60-763-374-87	Sequence 87, App1
34	217.5	16.7	252	7	US-11-268-554-118	Sequence 118, App
35	217.5	16.7	252	7	US-11-268-554-119	Sequence 119, App
36	217.5	16.7	252	7	US-11-342-366-1027	Sequence 1027, App
37	217.5	16.7	252	7	US-11-342-367-1027	Sequence 1027, App
38	193.5	14.8	595	8	US-60-772-265-1087	Sequence 1087, App
39	186	14.2	58	1	PCT-US05-42298-19	Sequence 19, App1
40	186	14.2	58	1	PCT-US05-34335-34	Sequence 34, App1
41	186	14.2	58	7	US-11-287-121A-19	Sequence 19, App1
42	180	13.8	352	6	US-10-567-867-1411	Sequence 1411, App
43	180	13.8	352	6	US-10-498-451-2681	Sequence 2681, App
44	162.5	12.4	2971	8	US-60-741-048-155	Sequence 155, App
45	162.5	12.4	2971	8	US-60-741-048-158	Sequence 158, App

## ALIGNMENTS

RESULT 1  
US-11-301-554-332  
Sequence 332, Application US/11301554  
GENERAL INFORMATION:  
APPLICANT: Henderson, Robert A.  
APPLICANT: Wang, Tonglong  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Kaloe, Michael D.  
APPLICANT: Sleath, Paul R.  
APPLICANT: Johnson, Jeffrey C.  
APPLICANT: Retter, Marc W.  
APPLICANT: Durham, Margarita  
APPLICANT: Carter, Darrick  
APPLICANT: Ranger, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: McNabb, Andria  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.478C21  
CURRENT APPLICATION NUMBER: US/11/301,554  
PRIOR FILING DATE: 2005-12-13  
PRIOR APPLICATION NUMBER: US 10/283,017  
PRIOR FILING DATE: 2002-10-28  
PRIOR APPLICATION NUMBER: US 10/113,872  
PRIOR FILING DATE: 2002-03-28  
PRIOR APPLICATION NUMBER: US 10/017,754  
PRIOR FILING DATE: 2001-10-29  
PRIOR APPLICATION NUMBER: US 09/902,941  
PRIOR FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: US 09/849,626  
PRIOR FILING DATE: 2001-05-03  
PRIOR APPLICATION NUMBER: US 09/736,457  
PRIOR FILING DATE: 2000-12-13  
PRIOR APPLICATION NUMBER: US 09/702,705  
PRIOR FILING DATE: 2000-10-30  
PRIOR APPLICATION NUMBER: US 09/677,419  
PRIOR FILING DATE: 2000-10-06  
PRIOR APPLICATION NUMBER: US 09/671,325  
PRIOR FILING DATE: 2000-09-26  
PRIOR APPLICATION NUMBER: US 09/658,824  
PRIOR FILING DATE: 2000-09-08  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 2157  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 332  
LENGTH: 235  
TYPE: PRT

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; ORGANISM: Homo sapiens
US-11-301-554-332

Query Match
Best Local Similarity 100.0%; Score 1306; DB 7; Length 235;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDAPRLGLSILLPLTEALGDAOEPTGNNAICLLPLDYGPCRALLLRYYDRYTOS 60
DB 1 MDAPRLGLSILLPLTEALGDAOEPTGNNAICLLPLDYGPCRALLLRYYDRYTOS 60
QY 61 CRQPLVGGCGEGNANNFYTWACDCAWRIEKVPKRLQVSDQCEGSTEKFFNLSM 120
DB 61 CRQPLVGGCGEGNANNFYTWACDCAWRIEKVPKRLQVSDQCEGSTEKFFNLSM 120
QY 121 TCCEFFSGGCHRRRIENRFPDEATCMGFCAPKKIISFCYSPKDEGLCSANVTYFNPRY 180
DB 121 TCCEFFSGGCHRRRIENRFPDEATCMGFCAPKKIISFCYSPKDEGLCSANVTYFNPRY 180
QY 181 RTCDATYTYGCGGNDNNPVSRDECKACAKALKKKKKMPRLRPSAIRIKRKQF 235
DB 181 RTCDATYTYGCGGNDNNPVSRDECKACAKALKKKKKMPRLRPSAIRIKRKQF 235

RESULT 2
US-11-107-643-1
; Sequence 1, Application US/11107643
; GENERAL INFORMATION:
; APPLICANT: Kistel, Walter
; TITLE OF INVENTION: Human Kunitz-type Inhibitor with Enhanced Antifibrinolytic
; FILE REFERENCE: 310.00170101
; CURRENT FILING DATE: 2005-04-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 213
; TYPE: PRT
; ORGANISM: homosapiens
US-11-107-643-1

Query Match
Best Local Similarity 91.9%; Score 1200; DB 7; Length 213;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 DAAOEPTGNNAICLLPLDYGPCRALLLRYYDRYTOSCRQPLVGGCGEGNANNFYTWAC 82
DB 1 DAAOEPTGNNAICLLPLDYGPCRALLLRYYDRYTOSCRQPLVGGCGEGNANNFYTWAC 60
QY 83 DDACWRIEKVPKRLQVSDQCEGSTEKFFNLSMTCEKFFSGGCHRRRIENRFPDE 142
DB 61 DDACWRIEKVPKRLQVSDQCEGSTEKFFNLSMTCEKFFSGGCHRRRIENRFPDE 120
QY 143 ATCMGFCAPKKIISFCYSPKDEGLCSANVTYFNPRYTCATYTYGCGGNDNNPVSR 202
DB 121 ATCMGFCAPKKIISFCYSPKDEGLCSANVTYFNPRYTCATYTYGCGGNDNNPVSR 180
QY 203 DCKRACAKALKKKKKMPRLRPSAIRIKRKQF 235
DB 181 DCKRACAKALKKKKKMPRLRPSAIRIKRKQF 213

RESULT 3
US-11-107-643-2
; Sequence 2, Application US/11107643
; GENERAL INFORMATION:
; APPLICANT: Kistel, Walter
; TITLE OF INVENTION: Human Kunitz-type Inhibitor with Enhanced Antifibrinolytic
; FILE REFERENCE: 310.00170101
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; CURRENT APPLICATION NUMBER: US/11/107,643
; CURRENT FILING DATE: 2005-04-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 73
; TYPE: PRT
; ORGANISM: homosapiens
US-11-107-643-2

Query Match
Best Local Similarity 32.2%; Score 421; DB 7; Length 73;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 DAAOEPTGNNAICLLPLDYGPCRALLLRYYDRYTOSCRQPLVGGCGEGNANNFYTWAC 82
DB 1 DAAOEPTGNNAICLLPLDYGPCRALLLRYYDRYTOSCRQPLVGGCGEGNANNFYTWAC 60
QY 83 DDACWRIEKVPKRV 95
DB 61 DDACWRIEKVPKRV 73

RESULT 4
US-11-107-643-3
; Sequence 3, Application US/11107643
; GENERAL INFORMATION:
; APPLICANT: Kistel, Walter
; TITLE OF INVENTION: Human Kunitz-type Inhibitor with Enhanced Antifibrinolytic
; FILE REFERENCE: 310.00170101
; CURRENT FILING DATE: 2005-04-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 73
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: mutated KD-1
US-11-107-643-3

Query Match
Best Local Similarity 32.0%; Score 418; DB 7; Length 73;
Matches 72; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 23 DAAOEPTGNNAICLLPLDYGPCRALLLRYYDRYTOSCRQPLVGGCGEGNANNFYTWAC 82
DB 1 DAAOEPTGNNAICLLPLDYGPCRALLLRYYDRYTOSCRQPLVGGCGEGNANNFYTWAC 60
QY 83 DDACWRIEKVPKRV 95
DB 61 DDACWRIEKVPKRV 73

RESULT 5
PCT-US05-42298-1
; Sequence 1, Application PC/TUS0542298
; GENERAL INFORMATION:
; APPLICANT: Dyax Corporation
; TITLE OF INVENTION: PLASMIN-INHIBITORY THERAPIES
; FILE REFERENCE: 10280-122W01
; CURRENT APPLICATION NUMBER: PCT/US05/42298
; CURRENT FILING DATE: 2005-11-22
; PRIOR FILING DATE: 2004-11-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 304
; TYPE: PRT
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/ ORGANISM: Homo sapiens  
PCT-US05-42298-1

Query Match 29.7%; Score 388; DB 1; Length 304;

Best Local Similarity 30.3%; Pred. No. 2.8e-30;  
Matches 86; Conservative 37; Mismatches 85; Indels 76; Gaps 8;

12 LILFLTEALGDAAOE-----PTGNNAEICLLPLDYGPCRALILRYYYDRYT 58  
17 LILNLAAPALNADSEDESHITITDTLPPLKLMHSFCAFKADDPCKAIMRFFFNIFT 76  
59 QSCROPLTGGCGGNANNTYWEACDCAWR-----TEKPKVCRLQVSDQ-- 105  
77 RCCEFTTGGCGGNRRFSLBECCKMCTRDNANRIKTTLOQKDPDFCLE--EDPGI 133  
106 CGSTETKTFPNLSMTCEKFFSGGCHRRNIENRFPDEATCMGFC----- 149  
134 CNGYITRYFNNQTKQCEKRFKYGGLGNM--NNFTLECKNI CEDGPNQVNDVYGTQ 191  
150 -----APKCI-----PSPCYSPKDEGLCSANTRYFNPRTTCAFTYTGCG 192  
192 NAVNNSLTPOSTKVPSLFEFHGSPWCLTPADRGCLCRANENRYYNSVIGKCRPFKYSGG 251  
193 GNDNNFVSRDECKRACAKAL-----KCKKPKLRAFA 224  
252 GNENNFTSKQECLECKKGFQIRISKGILIKTKRRKKQKVXIA 295

RESULT 6  
PCT-US05-34335-54

/ Sequence 54, Application PC/TUS0534335

/ GENERAL INFORMATION:

/ APPLICANT: Blait, Henry

/ APPLICANT: Beck, Thomas

/ APPLICANT: Lachner, Robert C.

/ TITLE OF INVENTION: KALLIKREIN INHIBITORS AND ANTI-THROMBOLYTIC AGENTS AND USES THEREOF

/ FILE REFERENCE: 10280-131W01

/ CURRENT APPLICATION NUMBER: PCT/US05/34335

/ CURRENT FILING DATE: 2005-09-22

/ PRIOR APPLICATION NUMBER: US 11/125,639

/ PRIOR FILING DATE: 2005-05-09

/ PRIOR APPLICATION NUMBER: US 10/953,902

/ PRIOR FILING DATE: 2004-09-27

/ NUMBER OF SEQ ID NOS: 56

/ SOFTWARE: FASTSEQ for Windows Version 4.0

/ SEQ ID NO 54

/ LENGTH: 304

/ TYPE: PRT

/ ORGANISM: Homo sapiens

PCT-US05-34335-54

Query Match 29.7%; Score 388; DB 1; Length 304;

Best Local Similarity 30.3%; Pred. No. 2.8e-30;  
Matches 86; Conservative 37; Mismatches 85; Indels 76; Gaps 8;

12 LILFLTEALGDAAOE-----PTGNNAEICLLPLDYGPCRALILRYYYDRYT 58  
17 LILNLAAPALNADSEDESHITITDTLPPLKLMHSFCAFKADDPCKAIMRFFFNIFT 76  
59 QSCROPLTGGCGGNANNTYWEACDCAWR-----TEKPKVCRLQVSDQ-- 105  
77 RCCEFTTGGCGGNRRFSLBECCKMCTRDNANRIKTTLOQKDPDFCLE--EDPGI 133  
106 CGSTETKTFPNLSMTCEKFFSGGCHRRNIENRFPDEATCMGFC----- 149  
134 CNGYITRYFNNQTKQCEKRFKYGGLGNM--NNFTLECKNI CEDGPNQVNDVYGTQ 191  
150 -----APKCI-----PSPCYSPKDEGLCSANTRYFNPRTTCAFTYTGCG 192  
192 NAVNNSLTPOSTKVPSLFEFHGSPWCLTPADRGCLCRANENRYYNSVIGKCRPFKYSGG 251  
193 GNDNNFVSRDECKRACAKAL-----KCKKPKLRAFA 224

DB 252 GNENNFTSKQECLECKKGFQIRISKGILIKTKRRKKQKVXIA 295

RESULT 7  
US-11-287-121A-1

/ Sequence 1, Application US/11287121A

/ GENERAL INFORMATION:

/ APPLICANT: Devy, Laetitia

/ APPLICANT: Ley, Arthur C.

/ APPLICANT: Lachner, Robert C.

/ TITLE OF INVENTION: PLASMIN-INHIBITORY THERAPIES

/ FILE REFERENCE: 10280-122001

/ CURRENT APPLICATION NUMBER: US/11/287,121A

/ CURRENT FILING DATE: 2005-11-22

/ PRIOR APPLICATION NUMBER: US 60/630,226

/ PRIOR FILING DATE: 2004-11-22

/ NUMBER OF SEQ ID NOS: 24

/ SOFTWARE: FASTSEQ for Windows Version 4.0

/ SEQ ID NO 1

/ LENGTH: 304

/ TYPE: PRT

/ ORGANISM: Homo sapiens

US-11-287-121A-1

Query Match 29.7%; Score 388; DB 7; Length 304;

Best Local Similarity 30.3%; Pred. No. 2.8e-30;  
Matches 86; Conservative 37; Mismatches 85; Indels 76; Gaps 8;

12 LILFLTEALGDAAOE-----PTGNNAEICLLPLDYGPCRALILRYYYDRYT 58  
17 LILNLAAPALNADSEDESHITITDTLPPLKLMHSFCAFKADDPCKAIMRFFFNIFT 76  
59 QSCROPLTGGCGGNANNTYWEACDCAWR-----TEKPKVCRLQVSDQ-- 105  
77 RCCEFTTGGCGGNRRFSLBECCKMCTRDNANRIKTTLOQKDPDFCLE--EDPGI 133  
106 CGSTETKTFPNLSMTCEKFFSGGCHRRNIENRFPDEATCMGFC----- 149  
134 CNGYITRYFNNQTKQCEKRFKYGGLGNM--NNFTLECKNI CEDGPNQVNDVYGTQ 191  
150 -----APKCI-----PSPCYSPKDEGLCSANTRYFNPRTTCAFTYTGCG 192  
192 NAVNNSLTPOSTKVPSLFEFHGSPWCLTPADRGCLCRANENRYYNSVIGKCRPFKYSGG 251  
193 GNDNNFVSRDECKRACAKAL-----KCKKPKLRAFA 224  
252 GNENNFTSKQECLECKKGFQIRISKGILIKTKRRKKQKVXIA 295

RESULT 8  
US-11-302-208-1

/ Sequence 1, Application US/11302208

/ GENERAL INFORMATION:

/ APPLICANT: Chen, Bao-Lu

/ APPLICANT: Huang, Chih-Yi

/ TITLE OF INVENTION: Stabilized Compositions Comprising Tissue Factor Pathway Inhibitor

/ FILE REFERENCE: 12441,00054

/ CURRENT APPLICATION NUMBER: US/11/302,208

/ CURRENT FILING DATE: 2005-12-14

/ PRIOR APPLICATION NUMBER: US/10/753,068

/ PRIOR FILING DATE: 2004-01-08

/ PRIOR APPLICATION NUMBER: US 60/438,519

/ PRIOR FILING DATE: 2003-01-08

/ PRIOR APPLICATION NUMBER: US 60/474,577

/ PRIOR FILING DATE: 2003-08-13

/ PRIOR APPLICATION NUMBER: US 60/509,260

/ PRIOR FILING DATE: 2003-10-08

/ PRIOR APPLICATION NUMBER: US 60/512,090

/ PRIOR FILING DATE: 2003-10-20

/ NUMBER OF SEQ ID NOS: 1

/ SOFTWARE: PatentIn version 3.1

/ SEQ ID NO 1

LENGTH: 276  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-302-208-1

Query Match 29.4%; Score 384.5; DB 7; Length 276;  
Best Local Similarity 31.6%; Pred. No. 5.5e-30;  
Matches 78; Conservative 35; Mismatches 71; Indels 63; Gaps 7;

QY 36 CLLEPLDYGPCCALLLRYRYDRYTQSCROFLYGCCEGANNFYTWACDDACMR-----88  
DB 26 CAFPADDGCKAIMKRFPPNIFRQCEBFIYGCCEGNNRFBELBECCKMCTRDNARI 85  
QY 89 ----LEKVRVCLQVSVDDQ--CEGSTEKYEFNLSMTCEKFPSCGCHRNRIENFPDE 142  
DB 86 KTTLQEKNDPFCFLE---EDPGICRGYITRYFYNNQTKQCEKFKYGGCLGNM--NNFETL 140  
QY 143 ATCMGFC-----APKTI-----PSFCYSPDGLCSA 169  
DB 141 BECKNICEDGPNQVNDYGTOLNANNLSLTPQSTKVPSLFEFHGSPWCLTPADRLGCPA 200  
QY 170 NTRYRYFNPRYATCDAFYTYGCGGNDNNFVSREDCRACAKAL-----KCKKK 217  
DB 201 NENRFFYNISVIGCKRPFKISGCGGNNFTSKQECIRACKKGFQIRISKGLIKTKRKK 260  
QY 218 MPELRPA 224  
DB 261 KQKVKIA 267

RESULT 9  
US-11-337-518-1  
Sequence 1, Application US/11337518

GENERAL INFORMATION:

APPLICANT: Arve, Bo H.  
APPLICANT: Dorn, Glenn J.  
APPLICANT: Patil, Gregory J.  
APPLICANT: Halenbeck, Robert F.  
APPLICANT: Johnson, Kirk  
APPLICANT: Chen, Bao-Ju  
APPLICANT: Bana, Risharan K.  
APPLICANT: Hora, Maninder S.  
APPLICANT: Madani, Hassan  
APPLICANT: Teang, Michael  
APPLICANT: Gustafson, Mark E.  
APPLICANT: Bidd, Gary S.  
APPLICANT: Johnson, Gary V.  
TITLE OF INVENTION: Formulation, Solubilization, Purification, and Refolding of Tissue  
FILE REFERENCE: 012441.00013  
CURRENT FILING DATE: 2006-01-24  
PRIOR APPLICATION NUMBER: US/09/996,588  
PRIOR FILING DATE: 2001-11-30  
PRIOR APPLICATION NUMBER: US 08/477,677  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: US 08/473,668  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: PCT/US96/09980  
PRIOR FILING DATE: 1996-06-07  
PRIOR APPLICATION NUMBER: US 09/973,211  
PRIOR FILING DATE: 1999-06-11  
PRIOR APPLICATION NUMBER: US 09/443,099  
PRIOR FILING DATE: 1999-11-18  
NUMBER OF SEQ ID NOS: 1  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 276  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-337-518-1

Query Match 29.4%; Score 384.5; DB 7; Length 276;

Best Local Similarity 31.6%; Pred. No. 5.5e-30;  
Matches 78; Conservative 35; Mismatches 71; Indels 63; Gaps 7;

QY 36 CLLEPLDYGPCCALLLRYRYDRYTQSCROFLYGCCEGANNFYTWACDDACMR-----88  
DB 26 CAFPADDGCKAIMKRFPPNIFRQCEBFIYGCCEGNNRFBELBECCKMCTRDNARI 85  
QY 89 ----LEKVRVCLQVSVDDQ--CEGSTEKYEFNLSMTCEKFPSCGCHRNRIENFPDE 142  
DB 86 KTTLQEKNDPFCFLE---EDPGICRGYITRYFYNNQTKQCEKFKYGGCLGNM--NNFETL 140  
QY 143 ATCMGFC-----APKTI-----PSFCYSPDGLCSA 169  
DB 141 BECKNICEDGPNQVNDYGTOLNANNLSLTPQSTKVPSLFEFHGSPWCLTPADRLGCPA 200  
QY 170 NTRYRYFNPRYATCDAFYTYGCGGNDNNFVSREDCRACAKAL-----KCKKK 217  
DB 201 NENRFFYNISVIGCKRPFKISGCGGNNFTSKQECIRACKKGFQIRISKGLIKTKRKK 260  
QY 218 MPELRPA 224  
DB 261 KQKVKIA 267

RESULT 10  
PCT-US05-42298-4  
Sequence 4, Application PC/TUS0542298

GENERAL INFORMATION:

APPLICANT: Dyak Corporation  
TITLE OF INVENTION: PLASMIN-INHIBITORY THERAPIES  
FILE REFERENCE: 10280-122W01  
CURRENT FILING DATE: PCT/US05/42298  
CURRENT FILING DATE: 2005-11-22  
PRIOR APPLICATION NUMBER: US 60/630,226  
PRIOR FILING DATE: 2004-11-22  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 58  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetically generated peptide  
PCT-US05-42298-4

Query Match 26.3%; Score 343; DB 1; Length 58;

Best Local Similarity 100.0%; Pred. No. 1.2e-26;  
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 NAEICLPLDYGPCCALLLRYRYDRYTQSCROFLYGCCEGANNFYTWACDDACMR 89  
DB 1 NAEICLPLDYGPCCALLLRYRYDRYTQSCROFLYGCCEGANNFYTWACDDACMR 58

RESULT 11  
PCT-US05-34335-37  
Sequence 37, Application PC/TUS0534335

GENERAL INFORMATION:

APPLICANT: Blait, Henry  
APPLICANT: Beck, Thomas  
APPLICANT: Ladner, Robert C.  
TITLE OF INVENTION: KALLIKREIN INHIBITORS AND ANTI-THROMBOLYTIC AGENTS AND USES THEREOF  
FILE REFERENCE: 10280-131W01  
CURRENT FILING DATE: PCT/US05/34335  
CURRENT FILING DATE: 2005-09-22  
PRIOR APPLICATION NUMBER: US 11/125,639  
PRIOR FILING DATE: 2005-05-09  
PRIOR APPLICATION NUMBER: US 10/953,902  
PRIOR FILING DATE: 2004-09-27  
NUMBER OF SEQ ID NOS: 56  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 37  
LENGTH: 58



TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetically generated peptide  
PCT-US05-34335-37

Query Match 26.3%; Score 343; DB 1; Length 58;  
Best Local Similarity 100.0%; Pred. No. 1.2e-26;  
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 NAEICLLPDIYGPCCALLLRYYDRYTQSCROFLYGCCEGNANFTYWEACDQACWRI 89  
Db 1 NAEICLLPDIYGPCCALLLRYYDRYTQSCROFLYGCCEGNANFTYWEACDQACWRI 58

RESULT 12  
US-11-287-121A-4  
Sequence 4, Application US/11287121A  
GENERAL INFORMATION:  
APPLICANT: Devy, Laetitia  
APPLICANT: Ley, Arthur C.  
APPLICANT: Ladner, Robert C.  
TITLE OF INVENTION: PLASMIN-INHIBITORY THERAPIES  
FILE REFERENCE: 10280-122001  
CURRENT APPLICATION NUMBER: US/11/287,121A  
CURRENT FILING DATE: 2005-11-22  
PRIOR APPLICATION NUMBER: US 60/630,226  
PRIOR FILING DATE: 2004-11-22  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 58  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetically generated peptide  
US-11-287-121A-4

Query Match 26.3%; Score 343; DB 7; Length 58;  
Best Local Similarity 100.0%; Pred. No. 1.2e-26;  
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 NAEICLLPDIYGPCCALLLRYYDRYTQSCROFLYGCCEGNANFTYWEACDQACWRI 89  
Db 1 NAEICLLPDIYGPCCALLLRYYDRYTQSCROFLYGCCEGNANFTYWEACDQACWRI 58

RESULT 13  
PCT-US05-42298-16  
Sequence 16, Application PC/TUS0542298  
GENERAL INFORMATION:  
APPLICANT: Dyax Corporation  
APPLICANT: Ley, Arthur C.  
APPLICANT: Ladner, Robert C.  
TITLE OF INVENTION: PLASMIN-INHIBITORY THERAPIES  
FILE REFERENCE: 10280-122001  
CURRENT APPLICATION NUMBER: PCT/US05/42298  
CURRENT FILING DATE: 2005-11-22  
PRIOR APPLICATION NUMBER: US 60/630,226  
PRIOR FILING DATE: 2004-11-22  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 16  
LENGTH: 61  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetically generated peptide  
PCT-US05-42298-16

Query Match 26.2%; Score 342; DB 1; Length 61;  
Best Local Similarity 100.0%; Pred. No. 1.6e-26;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 92 VPKVCLQVSDVDDQCGSTGTEKTFPNLSMTCKEFGGCHRRNIENRPFDEATCMGFCAP 151

Db 1 VPKVCLQVSDVDDQCGSTGTEKTFPNLSMTCKEFGGCHRRNIENRPFDEATCMGFCAP 60

Qy 152 K 152  
Db 61 K 61

RESULT 14  
PCT-US05-34335-38  
Sequence 38, Application PC/TUS0534335  
GENERAL INFORMATION:  
APPLICANT: Blair, Henry  
APPLICANT: Beck, Thomas  
APPLICANT: Ladner, Robert C.  
TITLE OF INVENTION: KALLIKREIN INHIBITORS AND ANTI-THROMBOLYTIC AGENTS AND USES THEREOF  
FILE REFERENCE: 10280-131001  
CURRENT APPLICATION NUMBER: PCT/US05/34335  
CURRENT FILING DATE: 2005-09-22  
PRIOR APPLICATION NUMBER: US 11/125,639  
PRIOR FILING DATE: 2005-05-09  
PRIOR APPLICATION NUMBER: US 10/953,902  
PRIOR FILING DATE: 2004-09-27  
NUMBER OF SEQ ID NOS: 56  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 38  
LENGTH: 61  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetically generated peptide  
PCT-US05-34335-38

Query Match 26.2%; Score 342; DB 1; Length 61;  
Best Local Similarity 100.0%; Pred. No. 1.6e-26;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 92 VPKVCLQVSDVDDQCGSTGTEKTFPNLSMTCKEFGGCHRRNIENRPFDEATCMGFCAP 151  
Db 1 VPKVCLQVSDVDDQCGSTGTEKTFPNLSMTCKEFGGCHRRNIENRPFDEATCMGFCAP 60

Qy 152 K 152  
Db 61 K 61

RESULT 15  
US-11-287-121A-16  
Sequence 16, Application US/11287121A  
GENERAL INFORMATION:  
APPLICANT: Devy, Laetitia  
APPLICANT: Ley, Arthur C.  
APPLICANT: Ladner, Robert C.  
TITLE OF INVENTION: PLASMIN-INHIBITORY THERAPIES  
FILE REFERENCE: 10280-122001  
CURRENT APPLICATION NUMBER: US/11/287,121A  
CURRENT FILING DATE: 2005-11-22  
PRIOR APPLICATION NUMBER: US 60/630,226  
PRIOR FILING DATE: 2004-11-22  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 16  
LENGTH: 61  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetically generated peptide  
US-11-287-121A-16

Query Match 26.2%; Score 342; DB 7; Length 61;  
Best Local Similarity 100.0%; Pred. No. 1.6e-26;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	92	VPKVCRLQVSVDDQCEGSTEKYPFNLSMTCEKFPFGGCHRNRIENRFPDDEATCMGFCAP	151
Db	1	VPKVCRLQVSVDDQCEGSTEKYPFNLSMTCEKFPFGGCHRNRIENRFPDDEATCMGFCAP	60
Qy	152	K 152	
Db	61	K 61	

Search completed: March 9, 2006, 20:08:42  
Job time : 40 secs



Db 1 GAGACCCCTTGGCCACCGGCGCCGCGACCCCTGACCAATGACCCCGCTCCCGCCCTGG 60  
Qy 61 GGGCTGCAATTCGTGCTGCTTTCTGACGAGAGGCTGCACTGGGCGATGCTGCTCAGAGC 120  
Db 61 GGGCTGCAATTCGTGCTGCTTTCTGACGAGAGGCTGCACTGGGCGATGCTGCTCAGAGC 120  
Qy 121 CAACGAGAAATACCGCGAGATCTGCTCTCCGCTGACGAGCCCTGCGGCGCC 180  
Db 121 CAACGAGAAATACCGCGAGATCTGCTCTCCGCTGACGAGCCCTGCGGCGCC 180  
Qy 181 TACTTCTCCGTTACTACTACGAGGTAACGAGAGGCTGCGGCGATGCTGCTGTA 240  
Db 181 TACTTCTCCGTTACTACTACGAGGTAACGAGAGGCTGCGGCGATGCTGCTGTA 240  
Qy 241 GCTGCGAGGCGACCGCAATTTCTACCTGGAGGCTTGGCAAGCTGCTGCTGTA 300  
Db 241 GCTGCGAGGCGACCGCAATTTCTACCTGGAGGCTTGGCAAGCTGCTGCTGTA 300  
Qy 301 GGAATGAAAAAGTTCCAAAGTTTCCGCGCTGCAAGTGAAGTGAAGCAAGTGAAG 360  
Db 301 GGAATGAAAAAGTTCCAAAGTTTCCGCGCTGCAAGTGAAGTGAAGCAAGTGAAG 360  
Qy 361 GGTCCACAGAAAGTAATTTCTTAATCTTAAGTTCATGATGCAATGTAATTTCTTTCCG 420  
Db 361 GGTCCACAGAAAGTAATTTCTTAATCTTAAGTTCATGATGCAATGTAATTTCTTTCCG 420  
Qy 421 GTGGGTGTCAACCGGAAACCGGATGGAAGAGGTTCCAGATGAACTGTTGATGAGCT 480  
Db 421 GTGGGTGTCAACCGGAAACCGGATGGAAGAGGTTCCAGATGAACTGTTGATGAGCT 480  
Qy 481 TCTGCGCACCAAGAAATTCATCTTTGCTACAGTCCAAAGATGAGGAGCTGCT 540  
Db 481 TCTGCGCACCAAGAAATTCATCTTTGCTACAGTCCAAAGATGAGGAGCTGCT 540  
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Db 721 GGAATAATTCGGAAGAGCAATTTTAAATCTTAATGATGCTGCTGCTGCTTATG 780  
Qy 781 GCTTAATTTGCTTATGCTGATCTGAAGATTAATGACAGCATGAGGAAACAAATCA 840  
Db 781 GCTTAATTTGCTTATGCTGATCTGAAGATTAATGACAGCATGAGGAAACAAATCA 840  
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Db 841 TTGGGATTTATTCACCAAGTTTATTAATCAAGTCACTTTTCAAAAAATTTGGAATTT 900  
Qy 901 TTTATATTAATCTGCTGCTAATGAAAGTGAAGTCACTTTTAAATTAATGCTGTAAC 960  
Db 901 TTTATATTAATCTGCTGCTAATGAAAGTGAAGTCACTTTTAAATTAATGCTGTAAC 960  
Qy 961 TGTGTTGAGAGTGAATTC 979  
Db 961 TGTGTTGAGAGTGAATTC 979

RESULT 2  
E34460 979 bp DNA linear PAT 31-JAN-2002  
LOCUS E34460  
DEFINITION Tissue factor pathway inhibitor-2 antibody.  
ACCESSION E34460

VERSION E34460.1 GI:18624347  
KEYWORDS JP 2000128803-A/1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE 1 (bases 1 to 979)  
AUTHORS Yui, Y.  
TITLE Tissue factor pathway inhibitor-2 antibody  
JOURNAL Patent: JP 2000128803-A 1 09-MAY-2000;  
SHIONOGI & CO LTD  
OS Homo sapiens (human)  
PN JP 2000128803-A/1  
PD 09-MAY-2000  
PR 19-OCT-1998 JP 1998296759  
PI YOSHIKI YUI  
PC A61K39/395, A61K39/395, A61K31/00, A61K31/00, C07K16/36, C12N5/10,  
PC C12N15/09,  
PC C12P21/02, G01N33/53, G01N33/53, G01N33/53, G01N33/53, G01N33/53,  
PC C12N15/00  
CC  
FH Key Location/Qualifiers  
CDS Location/Qualifiers  
1..979  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 100.0%; Score 979; DB 6; Length 979;  
Best Local Similarity 100.0%; Pred. No. 1, 6e-216;  
Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAGACCCCTTGGCCACCGGCGCCGCGACCCCTGACCAATGACCCCGCTCCCGCCCTGG 60  
Db 1 GAGACCCCTTGGCCACCGGCGCCGCGACCCCTGACCAATGACCCCGCTCCCGCCCTGG 60  
Qy 61 GGGCTGCAATTCGTGCTGCTTTCTGACGAGAGGCTGCACTGGGCGATGCTGCTCAGAGC 120  
Db 61 GGGCTGCAATTCGTGCTGCTTTCTGACGAGAGGCTGCACTGGGCGATGCTGCTCAGAGC 120  
Qy 121 CAACGAGAAATACCGCGAGATCTGCTCTCCGCTGACGAGCCCTGCGGCGCC 180  
Db 121 CAACGAGAAATACCGCGAGATCTGCTCTCCGCTGACGAGCCCTGCGGCGCC 180  
Qy 181 TACTTCTCCGTTACTACTACGAGGTAACGAGAGGCTGCGGCGATGCTGCTGTA 240  
Db 181 TACTTCTCCGTTACTACTACGAGGTAACGAGAGGCTGCGGCGATGCTGCTGTA 240  
Qy 241 GCTGCGAGGCGACCGCAATTTCTACCTGGAGGCTTGGCAAGCTGCTGCTGTA 300  
Db 241 GCTGCGAGGCGACCGCAATTTCTACCTGGAGGCTTGGCAAGCTGCTGCTGTA 300  
Qy 301 GGAATGAAAAAGTTCCAAAGTTTCCGCGCTGCAAGTGAAGTGAAGCAAGTGAAG 360  
Db 301 GGAATGAAAAAGTTCCAAAGTTTCCGCGCTGCAAGTGAAGTGAAGCAAGTGAAG 360  
Qy 361 GGTCCACAGAAAGTAATTTCTTAATCTTAAGTTCATGATGCAATGTAATTTCTTTCCG 420  
Db 361 GGTCCACAGAAAGTAATTTCTTAATCTTAAGTTCATGATGCAATGTAATTTCTTTCCG 420  
Qy 421 GTGGGTGTCAACCGGAAACCGGATGGAAGAGGTTCCAGATGAACTGTTGATGAGCT 480  
Db 421 GTGGGTGTCAACCGGAAACCGGATGGAAGAGGTTCCAGATGAACTGTTGATGAGCT 480  
Qy 481 TCTGCGCACCAAGAAATTCATCTTTGCTACAGTCCAAAGATGAGGAGCTGCTGCT 540  
Db 481 TCTGCGCACCAAGAAATTCATCTTTGCTACAGTCCAAAGATGAGGAGCTGCTGCT 540  
Qy 541 CTGCGCAATGTAATCTGCTAATTTTATTAATCAAGTAACTGTAATGCTTCACT 600

Db 541 CTGCCAATGTACTCGCTATTATTATTCAGAAATACAGAACCTGTATGCTTCACT 600  
 Qy 601 ATACTGCTGTGAGGAGGAAATGACATTAATTGTTAGAGGAGGATGCAAACTGAT 660  
 Db 601 ATACTGCTGTGAGGAGGAAATGACATTAATTGTTAGAGGAGGATGCAAACTGAT 660  
 Qy 661 GTGCAAAAGCTTTGAAAAAGAAAGAGATGCCAAAGCTTCGCTTTCAGATGAAATCC 720  
 Db 661 GTGCAAAAGCTTTGAAAAAGAAAGAGATGCCAAAGCTTCGCTTTCAGATGAAATCC 720  
 Qy 721 GGAATTTGCGAAGAGCAATTTTAAACATTCTTAATATGTCATCTTGTCTTTAG 780  
 Db 721 GGAATTTGCGAAGAGCAATTTTAAACATTCTTAATATGTCATCTTGTCTTTAG 780  
 Qy 781 GCTATTGCTCTTATGCTGTATCTGAAGAAATATATGACAGCATGAGAAACAAATCA 840  
 Db 781 GCTATTGCTCTTATGCTGTATCTGAAGAAATATATGACAGCATGAGAAACAAATCA 840  
 Qy 841 TTGGGATTTATTCACAGCTTTTATTAATCAAGTCACTTTTCAAAAATTTGGAATTT 900  
 Db 841 TTGGGATTTATTCACAGCTTTTATTAATCAAGTCACTTTTCAAAAATTTGGAATTT 900  
 Qy 901 TTTATATATACTAGCTGCTATTCAAATGTGAGTCTACCAATTTTAAATTATGTTCAAC 960  
 Db 901 TTTATATATACTAGCTGCTATTCAAATGTGAGTCTACCAATTTTAAATTATGTTCAAC 960  
 Qy 961 TGTTTGTGAGACTGAATTC 979  
 Db 961 TGTTTGTGAGACTGAATTC 979

## RESULT 3

LOCUS 114875 979 bp DNA linear PAT 02-APR-1996  
 DEFINITION Sequence 1 from patent US 5455338.  
 ACCESSION 114875  
 VERSION 114875.1 GI:1249784  
 KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 979)

AUTHORS Sprecher C.A., Kistiel, W. and Foster, D.C.

TITLE DNA encoding several human kunitz-type inhibitors and methods

JOURNAL relating Cherezo Patent/US 5455338-A 1 03-OCT-1995;

FEATURES Location/Qualifiers

1..979

/organism="unknown"

/mol\_type="unasigned DNA"

## ORIGIN

Query Match 100.0%; Score 979; DB 6; Length 979;

Best Local Similarity 100.0%; Pred. No. 1,66-216; Mismatches 0; Indels 0; Gaps 0;

Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAAGCTTGGCCAGCGGAGCGGCGCCGACCCCTGACACATGACCCGCTGCGCCCTTGG 60  
 Db 1 GGAAGCTTGGCCAGCGGAGCGGCGCCGACCCCTGACACATGACCCGCTGCGCCCTTGG 60  
 Qy 61 GGGCTGTGATTTCTGCTCTTTTCTGAGAGGCTGCACTGGGCGATCTGTCAGAGAC 120  
 Db 61 GGGCTGTGATTTCTGCTCTTTTCTGAGAGGCTGCACTGGGCGATCTGTCAGAGAC 120  
 Qy 121 CAACAGAAATACCGGAGATCTCTCTGCGCCCTGACATAAGGACCTGCGCGGCGCC 180  
 Db 121 CAACAGAAATACCGGAGATCTCTCTGCGCCCTGACATAAGGACCTGCGCGGCGCC 180  
 Qy 181 TACTTCTCCGTTACTACTACGACAGATACGCGAGAGCTGCGCGCAAGTTCTGTACGCGG 240  
 Db 181 TACTTCTCCGTTACTACTACGACAGATACGCGAGAGCTGCGCGCAAGTTCTGTACGCGG 240

Qy 241 GCTCGAGAGGCAACGCCAACATTTCTACACTGAGAGGCTTGGCAGCATGCTTGTGGA 300  
 Db 241 GCTCGAGAGGCAACGCCAACATTTCTACACTGAGAGGCTTGGCAGCATGCTTGTGGA 300  
 Qy 301 GGAATGAAAAAGTTCCCAAGTTTCCGGCTGCAAGTGAAGTGTGACACAGTGTAGG 360  
 Db 301 GGAATGAAAAAGTTCCCAAGTTTCCGGCTGCAAGTGAAGTGTGACACAGTGTAGG 360  
 Qy 361 GGTCCAGAAAGATATTTCTTAATCTTAATGTCATGATGATGATGATGATGATGATG 420  
 Db 361 GGTCCAGAAAGATATTTCTTAATCTTAATGTCATGATGATGATGATGATGATGATG 420  
 Qy 421 GTGGGTGTCAACCGAACCAGATGAGACAGATTTCCAGATGAGCTATGATGAGCT 480  
 Db 421 GTGGGTGTCAACCGAACCAGATGAGACAGATTTCCAGATGAGCTATGATGAGCT 480  
 Qy 481 TCTGCGCACCAAGAAATTCATCATTTTGTCTCAAGTCCAAAGATGAGGAGCTGTCT 540  
 Db 481 TCTGCGCACCAAGAAATTCATCATTTTGTCTCAAGTCCAAAGATGAGGAGCTGTCT 540  
 Qy 541 CTGCCAATGTACTCGCTATTATTATTCAGAAATACAGAACCTGTATGCTTCACT 600  
 Db 541 CTGCCAATGTACTCGCTATTATTATTCAGAAATACAGAACCTGTATGCTTCACT 600  
 Qy 601 ATACTGCTGTGAGGAGGAAATGACATTAATTGTTAGAGGAGGATGCAAACTGAT 660  
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 Qy 661 GTGCAAAAGCTTTGAAAAAGAAAGAGATGCCAAAGCTTCGCTTTCAGATGAAATCC 720  
 Db 661 GTGCAAAAGCTTTGAAAAAGAAAGAGATGCCAAAGCTTCGCTTTCAGATGAAATCC 720  
 Qy 721 GGAATTTGCGAAGAGCAATTTTAAACATTCTTAATATGTCATCTTGTCTTTAG 780  
 Db 721 GGAATTTGCGAAGAGCAATTTTAAACATTCTTAATATGTCATCTTGTCTTTAG 780  
 Qy 781 GCTATTGCTCTTATGCTGTATCTGAAGAAATATATGACAGCATGAGAAACAAATCA 840  
 Db 781 GCTATTGCTCTTATGCTGTATCTGAAGAAATATATGACAGCATGAGAAACAAATCA 840  
 Qy 841 TTGGGATTTATTCACAGCTTTTATTAATCAAGTCACTTTTCAAAAATTTGGAATTT 900  
 Db 841 TTGGGATTTATTCACAGCTTTTATTAATCAAGTCACTTTTCAAAAATTTGGAATTT 900  
 Qy 901 TTTATATATACTAGCTGCTATTCAAATGTGAGTCTACCAATTTTAAATTATGTTCAAC 960  
 Db 901 TTTATATATACTAGCTGCTATTCAAATGTGAGTCTACCAATTTTAAATTATGTTCAAC 960  
 Qy 961 TGTTTGTGAGACTGAATTC 979  
 Db 961 TGTTTGTGAGACTGAATTC 979

## RESULT 4

LOCUS 192685 979 bp DNA linear PAT 01-DEC-1998

DEFINITION Sequence 1 from patent US 5728674.

ACCESSION 192685 GI:3937155

VERSION 192685.1

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 979)

AUTHORS Sprecher C.A., Kistiel, W. and Foster, D.C.

TITLE Inhibition of blood coagulation by human-kunitz-type inhibitors

JOURNAL Patent/US 5728674-A 1 17-MAR-1998;

FEATURES Location/Qualifiers

1..979

/organism="unknown"

/mol\_type="unasigned DNA"

## ORIGIN

Query Match	100.0%;	Score 979;	DB 6;	Length 979;
Best Local Similarity	100.0%;	Pred. No. 1.6e-216;		
Matches 979; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

Qy	1	GGAGCGCCTTGGCCAGAGGGGGCCGCCGACCCCTCGACACTGACACCCCGCTGCCCCCTGG	60
Db	1	GGAGCGCTTGGCCAGAGGGGGCCGCCGACCCCTCGACACTGACACCCCGCTGCCCCCTGG	60
Qy	61	GGCTGTGCATTCTGCTCTTTTCTGACGGAAGGCTGCACTGGGCGATGTGTCTCAGAGC	120
Db	61	GGCTGTGCATTCTGCTCTTTTCTGACGGAAGGCTGCACTGGGCGATGTGTCTCAGAGC	120
Qy	121	CAACAAGAAATTAACGGGAGATGTGTCTCTGCCCCCTAATACTAGGACCCCTGCGGGGCC	180
Db	121	CAACAAGAAATTAACGGGAGATGTGTCTCTGCCCCCTAATACTAGGACCCCTGCGGGGCC	180
Qy	181	TACTTTCGCTTACTACTACGACAGGTACACGAGCTGCGCGACAGTTCCGTACGAGG	240
Db	181	TACTTTCGCTTACTACTACGACAGGTACACGAGCTGCGCGACAGTTCCGTACGAGG	240
Qy	241	GCTGCGAGGGCAACGCCCAATTTTCTACCTGGAGGGCTTTCGACGATGCTTCTGGA	300
Db	241	GCTGCGAGGGCAACGCCCAATTTTCTACCTGGAGGGCTTTCGACGATGCTTCTGGA	300
Qy	301	GGATAGAAAAAGTTCCCAAGTTTGGCCGCTGCAATGATGTGGAACGACAGTGTAGG	360
Db	301	GGATAGAAAAAGTTCCCAAGTTTGGCCGCTGCAATGATGTGGAACGACAGTGTAGG	360
Qy	361	GGTCCACAGAAAGATTTTCTTAACTTAAGTTCATGACATGTAAGAAAATTCCTTTCCG	420
Db	361	GGTCCACAGAAAGATTTTCTTAACTTAAGTTCATGACATGTAAGAAAATTCCTTTCCG	420
Qy	421	GTGGGTGTCAACCGAAACCGATTTGAGAACAGTTTTCAGATGACCTACCTGTATGGCT	480
Db	421	GTGGGTGTCAACCGAAACCGATTTGAGAACAGTTTTCAGATGACCTACCTGTATGGCT	480
Qy	481	TCGCGCACCAAGAAATTTCCATCATTTTGGCTACAGTCCAAAGATAGAGGACGTGGCT	540
Db	481	TCGCGCACCAAGAAATTTCCATCATTTTGGCTACAGTCCAAAGATAGAGGACGTGGCT	540
Qy	541	CTGCCAATGTGACTCGCTATTATTAAATTCAGAAATACAGAACTGTGATCTTTCACCT	600
Db	541	CTGCCAATGTGACTCGCTATTATTAAATTCAGAAATACAGAACTGTGATCTTTCACCT	600
Qy	601	ATATCTGCTGTGGAGGGAAATGACAAATATCTTTGTTACGAGGAGATTCGAAAGTGCAT	660
Db	601	ATATCTGCTGTGGAGGGAAATGACAAATATCTTTGTTACGAGGAGATTCGAAAGTGCAT	660
Qy	661	GTSCAAAAGCTTTGAAAAGAAAAAGAAAGATGCAAGAGCTTGCTTGSCCATGTGAATCC	720
Db	661	GTSCAAAAGCTTTGAAAAGAAAAAGAAAGATGCAAGAGCTTGCTTGSCCATGTGAATCC	720
Qy	721	GGAAAAATTCGGAAGAGCAATTTTAAACATTTCTAATATGTCAATCTTGTGTCTTAATG	780
Db	721	GGAAAAATTCGGAAGAGCAATTTTAAACATTTCTAATATGTCAATCTTGTGTCTTAATG	780
Qy	781	GCCTATTTCCTTAACTGTTTGTATCTGAGAAATATATGACAGCATGAGAAACAAATCA	840
Db	781	GCCTATTTCCTTAACTGTTTGTATCTGAGAAATATATGACAGCATGAGAAACAAATCA	840
Qy	841	TTTGATTTATTAATCAACAGTTTATTAATATCAAGTCACTTTTCAAAAAATTTGATTTT	900
Db	841	TTTGATTTATTAATCAACAGTTTATTAATATCAAGTCACTTTTCAAAAAATTTGATTTT	900
Qy	901	TTTATATATPACTAGCTGCTATTTCAATGTGAGTCAACATTTTAAATTAATTTATGGTCAAC	960
Db	901	TTTATATATPACTAGCTGCTATTTCAAAATGTGAGTCAACATTTTAAATTAATTTATGGTCAAC	960
Qy	961	TGTTTGTGAGACTGAATTC 979	
Db	961	TGTTTGTGAGACTGAATTC 979	

RESULT 5					
AR270815					
LOCUS	AR270815	979 bp	DNA	linear	PAT 10-APR-2003
DEFINITION	Sequence <u>1378</u> from patent US 6500938.				
ACCESSION	AR270815				
VERSION	AR270815.1 GI:29702049				
UPDATE DATE					

**ORIGIN**

Query March	100.0%	Score 979;	DB 6;	Length 979;
Best Local Similarity	100.0%	Pred. No. 1.6e-216;		
Matches 979;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	GGACGCGCTTGGCCCAAGGGGGCCGCCGACCCCTGACACCCCTGACCCCGCTGGCCCTCTGG	60
Db	1	GGAGCGCTTGGCCCAAGGGGGCCGCCGACCCCTGACACCCCTGACCCCGCTGGCCCTCTGG	60
QY	61	GGCTGTGCAATTCCTGCTGCTTTTCTGAGCGAGGGCTGCACTGGCGATCTGTCAAGAGC	120
Db	61	GGCTGTGCAATTCCTGCTGCTTTTCTGAGCGAGGGCTGCACTGGCGATCTGTCTCAAGAGC	120
QY	121	CAACAGAAATTAAGCCGAGATCTGTCTCTCCGCCCTTGAATCTAGGACCTTGCCTGGGCC	180
Db	121	CAACAGAAATTAAGCCGAGATCTGTCTCTGCCCTTGAATCTAGGACCTTGCCTGGGCC	180
QY	181	TACTTCTCCGTTACTACTACGACAGGTACAGCAGACCTGCGCAATTCCTGTACGGAG	240
Db	181	TACTTCTCCGTTACTACTACGAGGTACAGCAGACCTGCGCAATTCCTGTACGGAG	240
QY	241	GCTGCGAGGGGCAAGCCCAACATTTCTACACTGGAGGCTTGGCAGATGCTTGTCTGGA	300
Db	241	GCTGCGAGGGGCAAGCCCAACATTTCTACACTGGAGGCTTGGCAGATGCTTGTCTGGA	300
QY	301	GGATAGAAAAGTTCCCAAGTTTGGCGGCTGCAAGTAGTGATGAGCAACAAGTGAGG	360
Db	301	GGATAGAAAAGTTCCCAAGTTTGGCGGCTGCAAGTAGTGATGAGCAACAAGTGAGG	360
QY	361	GGTCCAAGAAAAGTATTTCTTTAATCTAAGTTCATGACATGTGAAAAATTCCTTTCCG	420
Db	361	GGTCCAAGAAAAGTATTTCTTTAATCTAAGTTCATGACATGTGAAAAATTCCTTTCCG	420
QY	421	GTGGGGGTCAACCGGAACCGGATTGAGAACAGGTTTCCAGATGAAAGCTATGTAAGGCT	480
Db	421	GTGGGGGTCAACCGGAACCGGATTGAGAACAGGTTTCCAGATGAAAGCTATGTAAGGCT	480
QY	481	TCTGCGCACAAAGAAAATTCATCATTTTGTCTACGTCCAAAAGATGAGGAGCTGTGCT	540
Db	481	TCTGCGCACAAAGAAAATTCATCATTTTGTCTACGTCCAAAAGATGAGGAGCTGTGCT	540
QY	541	CTGGCAATGTGACTGCGTAATTTTAATCCAAATACAGAACTGTGAAGCTTTCACT	600
Db	541	CTGGCAATGTGACTGCGTAATTTTAATCCAAATACAGAACTGTGAAGCTTTCACT	600
QY	601	ATACTGCTGTGAGAGGATGACATACTTTGTTACAGGAGAGATTCMAACGTGCAT	660
Db	601	ATACTGCTGTGAGAGGATGACATACTTTGTTACAGGAGAGATTCMAACGTGCAT	660
QY	661	GTGCAAAAGCTTTGAAAAAGAAAAAGAAAGATGCCAAAGCTTTCGCTTGCAGTAGAATCC	720
Db	661	GTGCAAAAGCTTTGAAAAAGAAAAAGAAAGATGCCAAAGCTTTCGCTTGCAGTAGAATCC	720

QY 721 GGAATTCGGAAGAGCAATTTTAAACAATTCTAATATGTCATCTGTTGCTTTATG 780  
 DB 721 GGAATTCGGAAGAGCAATTTTAAACAATTCTAATATGTCATCTGTTGCTTTATG 780  
 QY 781 GCTATTTGCTTTATGTTGTTATCTGAAGATTAATATGACAGATGAGAAACAATCA 840  
 DB 781 GCTATTTGCTTTATGTTGTTATCTGAAGATTAATATGACAGATGAGAAACAATCA 840  
 QY 841 TTGGTGATTTATTCACCAAGTTTATTAATACAGTCACTTTTCAAAAATTGGATTTT 900  
 DB 841 TTGGTGATTTATTCACCAAGTTTATTAATACAGTCACTTTTCAAAAATTGGATTTT 900  
 QY 901 TTTATATATTAATAGTCTGCTATTTCAAAATGAGTGTACCACTTTTAAATTATGTTCAAC 960  
 DB 901 TTTATATATTAATAGTCTGCTATTTCAAAATGAGTGTACCACTTTTAAATTATGTTCAAC 960  
 QY 961 TGTGTTGTGAGACTGAATTC 979  
 DB 961 TGTGTTGTGAGACTGAATTC 979

RESULT 6  
 AR437163 979 bp DNA linear PAT 18-DEC-2003  
 LOCUS AR437163  
 DEFINITION Sequence 1 from patent US 6656746.  
 ACCESSION AR437163  
 VERSION AR437163.1 GI:40200260  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 979)  
 Sprechter, C.A., Kistiel, W. and Foster, D.C.  
 Antibodies to human kunitz-type inhibitor  
 Patent: US 6656746-A 1 02-DEC-2003;  
 JOURNAL ZymoGenetics, Inc. and University of New Mexico; Seattle, WA  
 FEATURES  
 source 1..979  
 /organism="Unknown"  
 /mol\_type="genomic DNA"

## ORIGIN

Query Match 100.0%; Score 979; DB 6; Length 979;  
 Best Local Similarity 100.0%; Pred. No. 1,6e-216; Indels 0; Gaps 0;  
 Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGAAGCCTTGCCAGAGGCGCCGCGACCCCTGACACATGAGACCCCGCTCGCCCTTGG 60  
 DB 1 GGAAGCCTTGCCAGAGGCGCCGCGACCCCTGACACATGAGACCCCGCTCGCCCTTGG 60  
 QY 61 GAGCTGTGATTTGCTGCTTTTCTGACGAGAGCTGCACTGAGGAGATGCTGTCTCAGAGC 120  
 DB 61 GAGCTGTGATTTGCTGCTTTTCTGACGAGAGCTGCACTGAGGAGATGCTGTCTCAGAGC 120  
 QY 121 CAACGAGAAATTAACCGGAGATCTGCTCTGCGCCCTTAATACAGGACCTTCCCGGCGCC 180  
 DB 121 CAACGAGAAATTAACCGGAGATCTGCTCTGCGCCCTTAATACAGGACCTTCCCGGCGCC 180  
 QY 181 TACTTCTCCGTTACTACTACAGAGGTACAGGAGCTGCGCGCGAGTTCTGTATCGGGG 240  
 DB 181 TACTTCTCCGTTACTACTACAGAGGTACAGGAGCTGCGCGCGAGTTCTGTATCGGGG 240  
 QY 241 GCTGCGAGGGCAACCGCAATTTCTACACCTTGGAGGCTTTCGAGATGCTGTCTGAG 300  
 DB 241 GCTGCGAGGGCAACCGCAATTTCTACACCTTGGAGGCTTTCGAGATGCTGTCTGAG 300  
 QY 301 GGAATGAAAATTTCCCAAGTTTCCCGGCTGCAATGATGTGAGCAAGTGTGAGG 360  
 DB 301 GGAATGAAAATTTCCCAAGTTTCCCGGCTGCAATGATGTGAGCAAGTGTGAGG 360  
 QY 361 GGTCCACAGAAAAGATTTCTTAAATCTAAGTTCATGATGATGAAAATCTTTTCG 420  
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## RESULT 7

HUMHTFP 979 bp mRNA linear PRI 27-JUL-1994  
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 ACCESSION L27624  
 VERSION L27624.1 GI:441149  
 KEYWORDS tissue factor pathway inhibitor-2.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 REFERENCE 1 (bases 1 to 979)  
 Sprechter, C.A., Kistiel, W., Mathewes, S. and Foster, D.C.  
 Molecular cloning, expression, and partial characterization of a  
 second human tissue-factor-pathway inhibitor  
 Proc. Natl. Acad. Sci. U.S.A. 91 (8), 3353-3357 (1994)  
 PUBMED 8159751  
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Query Match 100.0%; Score 979; DB 8; Length 979;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-216;  
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 DB 961 TTTTGTGAGACTGAATTC 979

RESULT 8  
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 ACCESSION BC005330  
 VERSION BC005330.1 GI:13529109  
 KEYWORDS MGC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
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 Homiidae; Homo.  
 1 (bases 1 to 1203)  
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
 Klausner, R.D., Collins, P.S., Wagner, C.M., Shenmen, C.M., Schuler, G.D.,  
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
 Scheetz, T.E., Brownstein, M.J., Ugin, T.B., Toshiyuki, S.,  
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
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 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
 Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalins, D.B.,  
 Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
 Mammalian Gene Collection Program Team  
 Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
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 2 (bases 1 to 1203)

CONSRPT  
 TITLE  
 JOURNAL  
 PUBMED  
 REFERENCE  
 AUTHORS  
 CONSRPT  
 TITLE  
 JOURNAL  
 REMARK  
 COMMENT  
 NIH MGC Project  
 Direct Submission  
 Submitted (27-MAR-2001) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Bethesda, MD 20892-2590, USA  
 NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
 Contact: MGC help desk  
 Email: [gcgdb-remail.nih.gov](mailto:gcgdb-remail.nih.gov)  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome  
 Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web site: <http://www-shgc.stanford.edu>  
 Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R.  
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FEATURES  
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Query Match 100.0%; Score 979; DB 8; Length 1203;  
Best Local Similarity 100.0%; Pred. No. 1.6e-216; Indels 0; Gaps 0;  
Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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158  CAACAGAAATTAACCGGAGATCTGCTCCGCGCCCTGAGCTAGAGAGCCGCGCGGCGCC 217
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## ORIGIN

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DEFINITION Sequence 19662 from Patent WO0170979.  
ACCESSION CQ412591  
VERSION CQ412591.1 GI:41320372  
KEYWORDS

## SOURCE

Organism Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.

## REFERENCE

1 Lee, J. and Little, J.  
Genes, compositions, kits, and method for identification,  
assessment, prevention, and therapy of ovarian cancer  
Patent: WO 0170979-A 19662/27-SEP-2001;  
Millennium Pharmaceuticals Inc. (US)  
Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 1.6e-216; Indels 0; Gaps 0;  
Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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194  CAACAGAAATTAACCGGAGATCTGCTCCGCGCTGAGCTAGAGAGCCGCGCGGCGCC 253
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254  TACTTCTCGTTACTACTACAGAGTACACGAGAGCTGCGCGAGTCTCTGTAAGGAG 313
241  GCTGCGAGGCGCAACGCAATTTCTACACCTGCGAGGCTTTCGACAGATGCTTCTGGA 300
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LOCUS Sequence 3445 from Patent WO02068579.  
DEFINITION CQ717511  
ACCESSION CQ717511.1 GI:42278368  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
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Db 979 TGTTCGAGCTGAATTC 997

RESULT 11

AKI29833 2206 bp mRNA linear PRI 10-SEP-2003

LOCUS AKI29833

DEFINITION Homo sapiens cDNA FLJ26323 flk, clone HRT00813, highly similar to

ACCESSION AKI29833

VERSION AKI29833.1 GI:34526454

KEYWORDS oligo capping, flk (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1

AUTHORS Oca,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H., Suzuki,Y., Hara,H., Nakagawa,K., Mizuno,S., Morinaga,M., Kawamura,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Nishikawa,T., Sugiyama,A., Kawakami,B., Nagai,K., Isogai,T. and Sugano,S.

TITLE NEBO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2206)

AUTHORS Sugano,S. and Suzuki,Y.

TITLE Direct Submission

JOURNAL Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail: flicdn@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)

COMMENT NEBO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.

FEATURES

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1..2206

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/db\_xref="taxon:9606"

/clone="HRT00813"

/cfeature\_type="heart"

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/note="Cloning vector: pME18SFL3"

ORIGIN

Query Match 99.8%; Score 977.4; DB 8; Length 2206;

Best Local Similarity 99.9%; Pred.No.3.8e-216;

Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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2 GAGAGCCCTGGCCAGCGGGCGCGGAGCCCTGACACCATGAGCCCGCTGCGCCCTGG 60

3 GAGAGCCCTGGCCAGCGGGCGCGGAGCCCTGACACCATGAGCCCGCTGCGCCCTGG 97

61 GGCTGTGCAATTCCTGCTGCTGAGCGAGGCTGCACTGGGCGATGCTCTGAGAGC 120

98 GGCTGTGCAATTCCTGCTGCTGAGCGAGGCTGCACTGGGCGATGCTCTGAGAGC 157

121 CAAGAAGAAATTAAGCGGAGATGCTGCTGCTGAGCGAGGCTGAGAGCCCGCGGCGCC 180

158 CAAGAAGAAATTAAGCGGAGATGCTGCTGCTGAGCGAGGCTGAGAGCCCGCGGCGCC 217

181 TACTTCTCCGTACTACTACGACAGGTACAGCAGAGGCTGCGCGAGTCTCTGTACGGGG 240

218 TACTTCTCCGTACTACTACGACAGGTACAGCAGAGGCTGCGCGAGTCTCTGTACGGGG 277

241 GCTGCGAGGGCGAAGCGCAATTTCTACACCTGGAGAGGCTTGGACAGATCTTGTGGA 300

278 GCTGCGAGGGCGAAGCGCAATTTCTACACCTGGAGAGGCTTGGACAGATCTTGTGGA 337

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Qy 421 GTGGGTTCACCCGGAACCGGATTTGAAGACAGGTTTCCAGATGAAGTCTGTATGGGCT 480

Db 458 GTGGGTTCACCCGGAACCGGATTTGAAGACAGGTTTCCAGATGAAGTCTGTATGGGCT 517

Qy 481 TCTGCGACCAAGAAATTCATCATTTTGTCTACGTCCAAAGATGAGGACCTGTGCT 540

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Qy 541 CTGCGAATGTGACTGCTATTTATTTATTCAGATACAGAACTGTGATGCTTCACT 600

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Qy 601 ATACTGCTGTGAGGAGAAATGACATATCTTTGTACAGAGGAGATTTGCAAGTGCAT 660

Db 638 ATACTGCTGTGAGGAGAAATGACATATCTTTGTACAGAGGAGATTTGCAAGTGCAT 697

Qy 661 GTGCAAAAGCTTTGAAAGAAAGAAAGAGATGCAAGCTTGTGCTGCAAGTGCAT 720

Db 698 GTGCAAAAGCTTTGAAAGAAAGAAAGAGATGCAAGCTTGTGCTGCAAGTGCAT 757

Qy 721 GGAATAATTCGAGAGAACCAATTTTAAATTTTAAATGTGATCTTGTGCTTATG 780

Db 758 GGAATAATTCGAGAGAACCAATTTTAAATTTTAAATGTGATCTTGTGCTTATG 817

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Db 878 TTGCTGATTTATTCACAGATTTTATTAATTAATCAAGTCACTTTTCAAAAATTTGATTT 937

Qy 901 TTATATATATACAGTCTGATTCATTAATGAGTCTACATTTTAAATTAATGATCAAC 960

Db 938 TTATATATATACAGTCTGATTCATTAATGAGTCTACATTTTAAATTAATGATCAAC 997

Qy 961 TGTTCGAGCTGAATTC 979

Db 998 TGTTCGAGCTGAATTC 1016

RESULT 12

AY691946 1055 bp mRNA linear PRI 25-AUG-2004

LOCUS AY691946

DEFINITION Homo sapiens tissue factor pathway inhibitor 2 (TFPI2) mRNA,

ACCESSION AY691946

VERSION AY691946.1 GI:51475143

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1055)

AUTHORS Xu,Y., Li,T. and Du,G.

TITLE Direct Submission

JOURNAL Submitted (21-JUL-2004) Department of Molecular Biology, Medical Research Center, Shenzhen People's Hospital, Medical School of Jnan University, Dongmen North Road 1017, Shenzhen, Guangdong 518020, P.R. China

FEATURES

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/organism="Homo sapiens"

/mol\_type="mRNA"



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DB 559 CTGCCAATGTGACTGCTATTATTATTAAATCCAAAGATACAGAACTGTGATGCTTTCACCT 618  
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QY 661 GTGCMAAAGCTTTTGAAGAAAGAAAGATGCCAAAGCTTCCGTTTCCAGTAGAATCC 720  
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QY 721 GGAATAATTCGGAAGAGCAATTTTAAACATTTCTTAATATATGTCATCTTGTGCTTTAATG 780  
DB 739 GGAATAATTCGGAAGAGCAATTTTAAACATTTCTTAATATATGTCATCTTGTGCTTTAATG 798  
QY 781 GCTATTATTTGCTTTATGCTTGTATCTGAAAGATATATGACAGCATGAGAAACAAATCA 840  
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DB 919 TTTATATATTAATCTAGCTGCTATTCATATGATGAGTCTACCATTTTAAATTAATGTTTAC 978  
QY 961 TGTTTGTGAGACTGAT 977  
DB 979 TGTTTGTGAGACTGAT 995

RESULT 14  
LOCUS CS091788 1142 bp DNA linear PAT 03-JUN-2005  
DEFINITION Sequence 23 from Patent EP1533619.  
ACCESSION CS091788  
VERSION CS091788.1 GI:66949353  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1 Kochan, J.P. and Rosinski, J.A.  
AUTHORS Specific markers for metabolic syndrome  
TITLE Patent: EP 1533619-A 23 25-MAY-2005;  
JOURNAL F. Hoffmann-La Roche AG (CH)  
FEATURES  
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Best Local Similarity 99.7%; Pred. No. 66-215; 3; Indels 0; Gaps 0;

Match 974; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 919 TTTATATATTAATCTAGCTGCTATTCATATGATGAGTCTACCATTTTAAATTAATGTTTAC 978  
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DB 979 TGTTTGTGAGACTGAT 995

RESULT 15

HUMPS HUMPS 1142 bp mRNA linear PRI 11-JUN-1999  
LOCUS Homo sapiens mRNA for placental protein 5 (Pps), complete cds.  
DEFINITION D29992  
ACCESSION D29992.1 GI:484050  
VERSION  
KEYWORDS Pps; placental protein 5; serine proteinase inhibitor.

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ORGANISM    Homo sapiens
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.
REFERENCE   1 (bases 1 to 1142)
AUTHORS     Miyagi,Y., Koshikawa,N., Yasumitsu,H., Miyagi,E., Hirahara,F.,
            Aoki,I., Misugi,K., Umeda,M. and Miyazaki,K.
TITLE       cDNA cloning and mRNA expression of a serine proteinase inhibitor
            secreted by cancer cells: identification as placental protein 5 and
            tissue factor pathway inhibitor-2
JOURNAL     J. Biochem. 116 (5), 939-942 (1994)
PUBMED      789752
REFERENCE   2 (bases 1 to 1142)
AUTHORS     Miyagi,Y.
TITLE       Direct Submission
            Submitted (25-APR-1994) Yohel Miyagi, Yokohama City University,
            School of Medicine, Dept. of Pathology, Fukuura 3-9, Kanazawa-ku,
            Yokohama, Kanagawa 226, Japan (Tel:045-787-2587, Fax:045-786-0191)
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3'UTR
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polyA_signal 1031
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Query Match      99.3%; Score 972.2; DB 8; Length 1142;
Best Local Similarity 99.7%; Pred. No. 66-215;
Matches 974; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 319 GGATGAAAAAGTTCCAAAGTTGGCCGCTGCAGATGATGTGACGACAGTGTAGG 378
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Qy 421 GTGGGTGCACCGGAACCGGATTTGGAACAGGTTTCCAGATGACCTTGTATGGGCT 480
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Db 979 TGTTTGTAGACTGAAT 995

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 11, 2006, 05:23:21 ; Search time 632 Seconds  
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Title: US-10-800-057-1

Perfect score: 979

Sequence: 1 ggaagccttcgacagcagcggc.....ctgtttgagacgaattc 979

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: geneeqn2000a:\*
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- 8: geneeqn2005a:\*
- 9: geneeqn2006a:\*
- 10: geneeqn2007a:\*
- 11: geneeqn2008a:\*
- 12: geneeqn2009a:\*
- 13: geneeqn2010a:\*
- 14: geneeqn2011a:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	979	100.0	979	2	AAQ90469
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4	979	100.0	1172	6	ABV94764
5	979	100.0	2407	5	ADL45772
6	979	100.0	2540	8	ABX63609
7	979	100.0	2540	10	AD156337
8	977.4	99.8	1141	13	AD19178
9	977.2	99.3	1142	6	ABX76528
10	977.2	99.3	1142	8	ABX76328
11	977.2	99.3	1142	10	ABX08764
12	977.2	99.3	1142	11	ADN38705
13	977.2	99.3	1142	12	AD183254
14	977.2	99.3	1142	13	ADU06173
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23	618	63.1	619	8	ABZ20218	ABZ20218 Group III
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25	549.4	56.1	551	8	ABZ20262	ABZ20262 Group III
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27	512	52.3	535	8	ABZ20271	ABZ20271 Group III
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36	447	45.7	528	8	ACH10386	ACH10386 Human lun
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## ALIGNMENTS

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AC	AAQ90469;	
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DE	Kunitz-type inhibitor; protease-inhibitor; enzyme-inhibitor;	
XX	anticoagulant; deep vein thrombosis; TPPI-2; de.	
KW	Homo sapiens.	
XX		
OS		
XX		
FM	Key	Location/Qualifiers
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PF	02-NOV-1994;	94MO-US012609.
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FR	05-NOV-1993;	93US-00147710.
XX		
PA	(ZYMO ) ZYMOGENETICS INC.	
PA	(UYNE-) UNIV NEW MEXICO STATE.	
XX		
PI	Sprecher CA, Kistiel W, Foster DC;	
XX		
DR	WPI, 1995-193821/25.	
DR	P-PSDB; AAR74977.	
XX		
PT	Human Kunitz-type protease inhibitors - used as anticoagulants and in the	
PT	treatment of deep vein thrombosis.	
XX		
PS	Claim 4; Page 48; 65pp; English.	
XX		
CC	This DNA sequence allows for the production of human recombinant Kunitz-	
CC	type protease-inhibitor in large quantities that may be readily purified	

using known methods. The protein encoded by this sequence shares sequence homology and overall domain organization with tissue factor pathway-inhibitor (TFPI), and therefore has been designated TFPI-2

Sequence 979 BP; 258 A; 217 C; 231 G; 273 T; 0 U; 0 Other;

Query Match 100.0%; Score 979; DB 2; Length 979;  
Best Local Similarity 100.0%; Pred. No. 1.3e-257;  
Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GGCCTGCAATTCGTGCTTTTCTGACGAGAGCTGCACTGCGAGTGTGCTGCTCAGAGAC 120
DB 61 GGCCTGCAATTCGTGCTTTTCTGACGAGAGCTGCACTGCGAGTGTGCTGCTCAGAGAC 120
QY 121 CAACAGAAATTAACCGGAGATCTGCTCTGCGCCCTGACCTAGCAGACCCCTGCGGCGCC 180
DB 121 CAACAGAAATTAACCGGAGATCTGCTCTGCGCCCTGACCTAGCAGACCCCTGCGGCGCC 180
QY 181 TACTCTCGTACTACTACGACAGGTAACGAGAGCTGCGCGAGTTCTGTACGAGG 240
DB 181 TACTCTCGTACTACTACGACAGGTAACGAGAGCTGCGCGAGTTCTGTACGAGG 240
QY 241 GCTGCGAGGCGACGCGCAATTTCTACACTGCGAGGCTTTCGACAGATGCTTCTGGA 300
DB 241 GCTGCGAGGCGACGCGCAATTTCTACACTGCGAGGCTTTCGACAGATGCTTCTGGA 300
QY 301 GGAATGAAAAGTTCGCAAGTTTCCGCGTCAAGTGTGACGACGAGTGTGAGG 360
DB 301 GGAATGAAAAGTTCGCAAGTTTCCGCGTCAAGTGTGACGACGAGTGTGAGG 360
QY 361 GGTCCACAGAAAAGTATTTCTTAATCTAAGTTCATGACATGTAAGAAAATCTTTTCG 420
DB 361 GGTCCACAGAAAAGTATTTCTTAATCTAAGTTCATGACATGTAAGAAAATCTTTTCG 420
QY 421 GTGGGTGACCGGAAACCGGATGGAACAGGTTTCCAGATGACCTTGTATGAGGCT 480
DB 421 GTGGGTGACCGGAAACCGGATGGAACAGGTTTCCAGATGACCTTGTATGAGGCT 480
QY 481 TCTGGGCAACCAAGAAATTCATGTTTGTATGTAAGTTCGCAAGAAATGAGGAGCTGTGCT 540
DB 481 TCTGGGCAACCAAGAAATTCATGTTTGTATGTAAGTTCGCAAGAAATGAGGAGCTGTGCT 540
QY 541 CTGCCAATGTGACTGCTATTAATTTTAATCCAAAGATGAGAACTGTGATGCTTCACT 600
DB 541 CTGCCAATGTGACTGCTATTAATTTTAATCCAAAGATGAGAACTGTGATGCTTCACT 600
QY 601 ATACTGCGTGTGAGGAGATGCAATTAATTTTGAAGAGGAGATGCAAAAGCTGCAT 660
DB 601 ATACTGCGTGTGAGGAGATGCAATTAATTTTGAAGAGGAGATGCAAAAGCTGCAT 660
QY 661 GTGCAAAAGCTTTGAAAAGAAAAGAAAGATGCGCAACCTTGCCTTCCAGTGAATCC 720
DB 661 GTGCAAAAGCTTTGAAAAGAAAAGAAAGATGCGCAACCTTGCCTTCCAGTGAATCC 720
QY 721 GGAATAATTCGAAAGAAAGATTTTAACATTTTAATATGATCATTTGTTGCTTTAAG 780
DB 721 GGAATAATTCGAAAGAAAGATTTTAACATTTTAATATGATCATTTGTTGCTTTAAG 780
QY 781 GCTTATTTGCTTTATGTTGTATCTGAAGAAATTAATGACGATGAGAGAAACAAATCA 840
DB 781 GCTTATTTGCTTTATGTTGTATCTGAAGAAATTAATGACGATGAGAGAAACAAATCA 840
QY 841 TTGGGATTTATTCACGATTTTATTAATCAAGTCACTTTTCAAAAATTTGATTTT 900
DB 841 TTGGGATTTATTCACGATTTTATTAATCAAGTCACTTTTCAAAAATTTGATTTT 900
QY 901 TTATATATTAATAGTCTGATTTCAATATGATGATGATGATGATGATGATGATGATGAT 960
DB 901 TTATATATTAATAGTCTGATTTCAATATGATGATGATGATGATGATGATGATGATGAT 960

```

QY 961 TGTGTGAGACTGAATTC 979  
DB 961 TGTGTGAGACTGAATTC 979

RESULT 2  
ACAS6780  
ID ACAS6780 standard; cDNA; 979 BP.

ACAS6780;

06-JUN-2003 (first entry)

Human signalling pathway polynucleotide probe SEQ ID NO 1378.

Human; probe; ss; array element; Parkinson's disease;

signalling pathway population; cancer; adenocarcinoma; leukemia;

immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.

Homo sapiens.

US6500938-B1.

30-JAN-1998; 98US-00016434.

30-JAN-1998; 98US-00016434.

(INCYTE) INCYTE GENOMICS INC.

Au-Young J, Seilhamer JJ;

WPI, 2003-352189/33.

Combination of polynucleotide probes, useful as array elements in a

microarray for monitoring the expression of a number of target

polynucleotides.

Claim 1; SEQ ID NO 1378; 65pp; English.

The invention relates to a combination which, comprises a number of

polynucleotide probes comprising a sequence selected from one of the 1490

sequences mentioned in the specification. The combination is useful as an

array element in a microarray for monitoring the expression of a number

of target polynucleotides. The microarray is particularly useful in the

diagnosis and treatment of cancer and immunopathology and neuropathology.

The microarray is useful in diagnostics and treatment regimens, drug

discovery and development, toxicological and carcinogenicity studies,

forensics and pharmacogenomics. The microarray is also useful for

monitoring progression of diseases and for developing sophisticated

profiles for the effects of currently available therapeutic drugs. The

combination is also useful for purifying a subpopulation of mRNAs, cDNAs

and genomic fragments and in research and diagnostic applications. The

array can detect changes in expression in a large number of genes coding

for different signalling pathway populations which can be used to diagnose

various diseases including cancer e.g. adenocarcinoma and leukemia,

immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease

and Parkinson's disease. The present sequence represents a polynucleotide

probe of the invention. Note: The sequence data for this patent did not

form part of the printed specification but was obtained in electronic

format directly from USPTO at

seqdata.uspto.gov/sequence.html?docID=06500938B1

Sequence 979 BP; 258 A; 217 C; 231 G; 273 T; 0 U; 0 Other;

Query Match 100.0%; Score 979; DB 10; Length 979;

Best Local Similarity 100.0%; Pred. No. 1.3e-257;

Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GGACGCGCTTGGCCGAGGCGCGCCGACCCCTGACGACATGAGACCCCGCTGCGCCCTGCG 60



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Db      1  GAGAGCCTTGGCCAGCGGCGCGCCGACCCCTGACCATGAGCCCGCTGCGCCCTTGG  60
Qy      61  GGGTGTGCAATTCGTGCTTTTCTGAGAGGAGGCTGCACTGGGCGATGCTGTCAAGAGC  120
Db      61  GGGTGTGCAATTCGTGCTTTTCTGAGAGGAGGCTGCACTGGGCGATGCTGTCAAGAGC  120
Qy     121  CAACAGAAATTAACGCGAGATCTGTCTGCGCCCTGAGCTAGCGAGCCCTGCGGGGCC  180
Db     121  CAACAGAAATTAACGCGAGATCTGTCTGCGCCCTGAGCTAGCGAGCCCTGCGGGGCC  180
Qy     181  TACTTCTCCGTTACTACTAGCAGAGTAACGAGAGCTGCGCGAGTTCCTGTACGGGG  240
Db     181  TACTTCTCCGTTACTACTAGCAGAGTAACGAGAGCTGCGCGAGTTCCTGTACGGGG  240
Qy     241  GCTGCGAGAGGCAAGCCCAACATTTCTACACTGGGAGGCTTGGCAAGATGTTGCTGGA  300
Db     241  GCTGCGAGAGGCAAGCCCAACATTTCTACACTGGGAGGCTTGGCAAGATGTTGCTGGA  300
Qy     301  GGAATGAAAAAGTTCCCAAGTTTGCAGGCTGCAAGTGAAGTGAAGCAAGTGAAGG  360
Db     301  GGAATGAAAAAGTTCCCAAGTTTGCAGGCTGCAAGTGAAGTGAAGCAAGTGAAGG  360
Qy     361  GGTCCACAGAAAAGTATTTCTTAATCTAAGTTCAGTGAAGTGAAGTGAAGTGAAG  420
Db     361  GGTCCACAGAAAAGTATTTCTTAATCTAAGTTCAGTGAAGTGAAGTGAAGTGAAG  420
Qy     421  GTGGGTGTCACCGGAAACCGGATGGAACAGGTTTCCAGATGAAGTCTGTATGGGCT  480
Db     421  GTGGGTGTCACCGGAAACCGGATGGAACAGGTTTCCAGATGAAGTCTGTATGGGCT  480
Qy     481  TCTGGGCAACCAAGAAAATTCATCATTTTGTCTACAGTCCAAAAGATGAGGAGCTGT  540
Db     481  TCTGGGCAACCAAGAAAATTCATCATTTTGTCTACAGTCCAAAAGATGAGGAGCTGT  540
Qy     541  CTGCCAATGTAAGTCTGTAATTAATTAATCCAGATGAGAACTGTGATGCTTCACT  600
Db     541  CTGCCAATGTAAGTCTGTAATTAATTAATCCAGATGAGAACTGTGATGCTTCACT  600
Qy     601  ATACTGCTGTGAGAGGAAATGACATACTTTGTGACAGGAGAGATGCAAAAGCTGAT  660
Db     601  ATACTGCTGTGAGAGGAAATGACATACTTTGTGACAGGAGAGATGCAAAAGCTGAT  660
Qy     661  GTGCAAAAGCTTTGAAAAAGAAAAGAGATGCCAAGCTTGCCTTTCAGATAGATCC  720
Db     661  GTGCAAAAGCTTTGAAAAAGAAAAGAGATGCCAAGCTTGCCTTTCAGATAGATCC  720
Qy     721  GGAATAATTCGAAAGAGCAATTTTAACATTTCTTAATATGTCATCTGTGTTCTTATG  780
Db     721  GGAATAATTCGAAAGAGCAATTTTAACATTTCTTAATATGTCATCTGTGTTCTTATG  780
Qy     781  GCTTATTTGCTTATGTTGTTATCTGAAGATTAATGACAGCATGAGAAACAAATCA  840
Db     781  GCTTATTTGCTTATGTTGTTATCTGAAGATTAATGACAGCATGAGAAACAAATCA  840
Qy     841  TTGGGATTTATTCACAGTTTATTAATTAACAATCACTTTTCAAAAATTTGATTTT  900
Db     841  TTGGGATTTATTCACAGTTTATTAATTAACAATCACTTTTCAAAAATTTGATTTT  900
Qy     901  TTTATATATTAATTAATGCTGATTAATTAATGATGATGATGATGATGATGATGAT  960
Db     901  TTTATATATTAATTAATGCTGATTAATTAATGATGATGATGATGATGATGATGAT  960
Qy     961  TGTGTTGAGAGTGAATTC  979
Db     961  TGTGTTGAGAGTGAATTC  979

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DT      22-APR-2004 (first entry)
XX
DE      Human polynucleotide probe #1378.
XX
KW      Human; probe; se; receptor-like polypeptide; transducing polypeptide;
KW      effector-like polypeptide; cancer; immunopathology; neuropathology;
KW      drug development; toxicology; carcinogenicity;
KW      signalling pathway polypeptide; adrenal gland; bladder; bone;
KW      bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS;
KW      diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology;
KW      dementia; amnesia; epilepsy; Alzheimer's disease; depression.
XX
OS      Homo sapiens.
XX
PN      US2004010136-A1.
XX
PD      15-JAN-2004.
XX
PF      26-NOV-2002; 2002US-00305720.
XX
PR      30-JAN-1998; 98US-00016434.
XX
PA      (INCY-) INCYTE GENOMICS INC.
XX
PI      Au-Young J, Sellhammer JJ;
XX
DR      WPI; 2004-090520/09.
XX
PT      New composition comprising polynucleotide probes, useful as array
PT      elements in a microarray for monitoring the expression of target
PT      polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic
PT      fragments.
XX
PS      Claim 6; SEQ ID NO 1378; 73pp; English.
XX
CC      The invention relates to a composition of polynucleotide probes
CC      comprising first polynucleotide probes comprising at least a portion of a
CC      gene encoding a receptor-like polypeptide, second polynucleotide probes
CC      comprising at least a portion of a gene encoding a transducing
CC      polypeptide and third polynucleotide probes comprising at least a portion
CC      of a gene encoding an effector-like polypeptide. The probes of the
CC      composition are useful as array elements in a microarray for monitoring
CC      the expression of target polynucleotides. The microarray is useful in the
CC      diagnosis and treatment of cancer, an immunopathology or a
CC      neuropathology. It can also be used for drug discovery and development.
CC      Microarrays can also be used for monitoring the progression of diseases.
CC      that may be associated with the altered expression of signalling pathway
CC      polypeptides. The composition can also be used to purify a subpopulation
CC      of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile
CC      is also useful for the diagnosis and treatment of cancer, e.g. cancers of
CC      the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,
CC      an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or
CC      ulcerative colitis, or a neuropathology, e.g. dementia, amnesia,
CC      epilepsy, Alzheimer's disease or depression. This sequence represents a
CC      human polynucleotide probe of the invention. Note: The sequence data for
CC      this patent did not form part of the printed specification but was
CC      obtained in electronic format directly from USPTO at
CC      seqdata.uspto.gov/sequence.html.
XX
SQ      Sequence 979 BP; 258 A; 217 C; 231 G; 273 T; 0 U; 0 Other;

```

Query Match 100.0%; Score 979; DB 12; Length 979;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-257;  
 Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1  GAGAGCCTTGGCCAGCGGCGCGCCGACCCCTGACCATGAGCCCGCTGCGCCCTTGG  60
Db      1  GAGAGCCTTGGCCAGCGGCGCGCCGACCCCTGACCATGAGCCCGCTGCGCCCTTGG  60
Qy     61  GGGTGTGCAATTCGTGCTTTTCTGAGAGGAGGCTGCACTGGGCGATGCTGTCAAGAGC  120
Db     61  GGGTGTGCAATTCGTGCTTTTCTGAGAGGAGGCTGCACTGGGCGATGCTGTCAAGAGC  120

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QY 121 CAACAGAAATTAACCGGAGATCTGTCTCTGCCCCCTAGACTACGAGACCTGCGGAGCC 180
DB 121 CAACAGAAATTAACCGGAGATCTGTCTCTGCCCCCTAGACTACGAGACCTGCGGAGCC 180
QY 181 TACTTCTCCGTTACTACTACGAGGTACACGAGAGCTGCGGAGCTCTGTACGGGG 240
DB 181 TACTTCTCCGTTACTACTACGAGGTACACGAGAGCTGCGGAGCTCTGTACGGGG 240
QY 241 GCTGCGAGGGCAACGCAACATTTCTACACCTGGAGGGCTTGGACGATGTCTGCTGA 300
DB 241 GCTGCGAGGGCAACGCAACATTTCTACACCTGGAGGGCTTGGACGATGTCTGCTGA 300
QY 301 GGATAGAAAAAGTCTCCAAAGTTTCCGGCTGCAAGTAGGTGAGCAGCAGTGTGAGG 360
DB 301 GGATAGAAAAAGTCTCCAAAGTTTCCGGCTGCAAGTAGGTGAGCAGCAGTGTGAGG 360
QY 361 GGTCCACAGAAAAAGTATTTCTTAAATCTAAGTTCATGACATGTGAAAAATTTCTTTCGG 420
DB 361 GGTCCACAGAAAAAGTATTTCTTAAATCTAAGTTCATGACATGTGAAAAATTTCTTTCGG 420
QY 421 GTGGGTGTCAACCGGAACCGGATTTGAGAACGGTTCCAGATGACCTATGTAAGGGCT 480
DB 421 GTGGGTGTCAACCGGAACCGGATTTGAGAACGGTTCCAGATGACCTATGTAAGGGCT 480
QY 481 TCTGCGCACCAAGAAAAATTCATCATTTTGTGCTACAGTCCAAAAGATGAGGAGCTGTGCT 540
DB 481 TCTGCGCACCAAGAAAAATTCATCATTTTGTGCTACAGTCCAAAAGATGAGGAGCTGTGCT 540
QY 541 CTGCGCAATGTGACTGCTATTTATTTTAAATCCAAAGTACAGAACTGTGATGCTTTCACTT 600
DB 541 CTGCGCAATGTGACTGCTATTTATTTTAAATCCAAAGTACAGAACTGTGATGCTTTCACTT 600
QY 601 ATACTGCTGTGAGGAGATGACATTAATCTTGTAGCAGGAGGATTCAGAACGTGCAT 660
DB 601 ATACTGCTGTGAGGAGATGACATTAATCTTGTAGCAGGAGGATTCAGAACGTGCAT 660
QY 661 GTGCAAAAGCTTTGAAAAAGAAAAAGAGATCCAAAGCTTGTGCTGCAAGTAAATCC 720
DB 661 GTGCAAAAGCTTTGAAAAAGAAAAAGAGATCCAAAGCTTGTGCTGCAAGTAAATCC 720
QY 721 GGAATATTCGGAAGAGCAATTTTAAACATTTTAAATGTCATCTTGTGTCTTATG 780
DB 721 GGAATATTCGGAAGAGCAATTTTAAACATTTTAAATGTCATCTTGTGTCTTATG 780
QY 781 GCTTATTTGCTTATGTTGATGTCGAAGATTAATATGACAGATGAGGAAAAATCA 840
DB 781 GCTTATTTGCTTATGTTGATGTCGAAGATTAATATGACAGATGAGGAAAAATCA 840
QY 841 TTGCTGATTTATTCACAGTTTATTAATACAGTCACTTTTCAAAAATTTGATTTT 900
DB 841 TTGCTGATTTATTCACAGTTTATTAATACAGTCACTTTTCAAAAATTTGATTTT 900
QY 901 TTTATATTAATTAAGTCTATTCAAATGTGAGTCTACCATTTTAAATTAATGTTCAAC 960
DB 901 TTTATATTAATTAAGTCTATTCAAATGTGAGTCTACCATTTTAAATTAATGTTCAAC 960
QY 961 TGTGTGTGAGTGAATTC 979
DB 961 TGTGTGTGAGTGAATTC 979

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RESULT 4  
ID ABV94764 standard; cDNA; 1172 BP.  
ABV94764;

14-JAN-2003 (first entry)

Human pancreatic cancer expressed cDNA SEQ ID NO 145.

Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;

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KW cytosolic; tumour; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200260317-A2.
XX
PD 08-AUG-2002.
XX
PF 30-JAN-2002; 2002WO-US002781.
XX
PR 30-JAN-2001; 2001US-0265305P.
PR 31-JAN-2001; 2001US-0265682P.
PR 09-FEB-2001; 2001US-0267568P.
PR 21-MAR-2001; 2001US-0278651P.
PR 28-APR-2001; 2001US-0287112P.
PR 16-MAY-2001; 2001US-0291631P.
PR 12-JUL-2001; 2001US-0305484P.
PR 20-AUG-2001; 2001US-0313999P.
PR 27-NOV-2001; 2001US-0333626P.
PA (CORI-) CORIXA CORP.
PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
XX
XX WPI; 2002-627435/67.
XX P-P5DB; ABP68618.
XX
PT New isolated polynucleotide and pancreatic tumor polypeptides, useful for
PT diagnosing, preventing and/or treating cancer, particularly pancreatic
PT cancer.
PS Claim 1; SEQ ID NO 145; 300pp + Sequence Listing; English.
XX
XX The invention relates to an isolated polynucleotide (I) comprising: (a)
XX any of a group of over 4000 nucleotide sequences (ABV94628-ABV9145); (b)
XX complements of (a); (c) sequences consisting of at least 20 contiguous
XX residues of (a); (d) sequences that hybridize to (a), under moderately
XX stringent conditions; (e) sequences having at least 75% or 90% identity
XX to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
XX ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
XX in a patient and compositions comprising polypeptides, polynucleotides,
XX antibodies, fusion proteins, T cell populations and antigen presenting
XX cells expressing the polypeptide are useful in treating pancreatic cancer
XX and stimulating an immune response. The polynucleotides can be used as
XX probes or primers for nucleic acid hybridisation, in the design and
XX preparation of ribozyme molecules for inhibiting expression of the tumour
XX polypeptides and proteins in the tumour cells, in vaccines and for gene
XX therapy. Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
SQ
Sequence 1172 BP; 329 A; 258 C; 263 G; 322 T; 0 U; 0 Other;
Query Match 100.0%; Score 979; DB 6; Length 1172;
Beet Local Similarity 100.0%; Pred. No. 1.4e-257;
Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GAGAGCCTTGGCCAGCGGGCGCCGACCCCTGACCAATGAGACCCGCTGCGCCCTTGG 60
DB 38 GAGAGCCTTGGCCAGCGGGCGCCGACCCCTGACCAATGAGACCCGCTGCGCCCTTGG 97
QY 61 GGCTGTGATTTCTGTGCTTTTCTGACGAGGTGCACTGGGCGATGCTGCTACAGAGC 120
DB 98 GGCTGTGATTTCTGTGCTTTTCTGACGAGGTGCACTGGGCGATGCTGCTACAGAGC 157
QY 121 CAACAGAAATTAAGCGGAGATGTGTCTCTGCCCCCTAGACTACGAGACCTGCGGAGCC 180
DB 158 CAACAGAAATTAAGCGGAGATGTGTCTCTGCCCCCTAGACTACGAGACCTGCGGAGCC 217
QY 181 TACTTCTCCGTTACTACTACGAGGTACACGAGAGCTGCGGAGCTCTGTACGGGG 240
DB 218 TACTTCTCCGTTACTACTACGAGGTACACGAGAGCTGCGGAGCTCTGTACGGGG 277

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QY 241 GGTGGAGGCGCAACCAATTTCTACCTGGAGGCTTGCAGCAATGCTTGTGGA 300  
 DB 314 GCTGGAGGCGCAACCAATTTCTACCTGGAGGCTTGCAGCAATGCTTGTGGA 373  
 QY 301 GGAATGAAAAAGTTTCCCAAGTTTGCCTGCAAGTGAAGTGAAGCAAGTGAAG 360  
 DB 374 GGAATGAAAAAGTTTCCCAAGTTTGCCTGCAAGTGAAGTGAAGCAAGTGAAG 433  
 QY 361 GGTCCAGAAAAAGTATTTCTTAAATCTAAGTTCAGTGAATGAAAAATTTCTTTCCG 420  
 DB 434 GGTCCAGAAAAAGTATTTCTTAAATCTAAGTTCAGTGAATGAAAAATTTCTTTCCG 493  
 QY 421 GTGGGTTCACCGGAAACCGGATTTGAGAACAGTTTCCAGATGAACCTACTTGTATGGCT 480  
 DB 494 GTGGGTTCACCGGAAACCGGATTTGAGAACAGTTTCCAGATGAACCTACTTGTATGGCT 553  
 QY 481 TCTGGGCAACCAAGAAAAATTCATCATTTTGTCTACAGTCCAAAAAGATGAGGAGCTGTGCT 540  
 DB 554 TCTGGGCAACCAAGAAAAATTCATCATTTTGTCTACAGTCCAAAAAGATGAGGAGCTGTGCT 613  
 QY 541 CTGCCAATGTGACTGCTATTAATTTAAATCCAAAGTACAGAACTGTGATGCTTTCACT 600  
 DB 614 CTGCCAATGTGACTGCTATTAATTTAAATCCAAAGTACAGAACTGTGATGCTTTCACT 673  
 QY 601 ATACTGCTGTGAGAGGAATGACATACTTTGTAGAGGAGGATTTGCAAAAGCTGCAT 660  
 DB 674 ATACTGCTGTGAGAGGAATGACATACTTTGTAGAGGAGGATTTGCAAAAGCTGCAT 733  
 QY 661 GTGCAAAAGCTTTGAAAAAGAAAAAGAAATGCAAAAGCTTGTGCAAGTACATCC 720  
 DB 734 GTGCAAAAGCTTTGAAAAAGAAAAAGAAATGCAAAAGCTTGTGCAAGTACATCC 793  
 QY 721 GGAATAATTCGAAAGAAAGCAATTTAAACATTTTAATATGTCATCTTGTGTCTTTATG 780  
 DB 794 GGAATAATTCGAAAGAAAGCAATTTAAACATTTTAATATGTCATCTTGTGTCTTTATG 853  
 QY 781 GCTATTTTGCCTTTATGTTGATCTGAAGAAATATATGACGATGAGAAACAAATCA 840  
 DB 854 GCTATTTTGCCTTTATGTTGATCTGAAGAAATATATGACGATGAGAAACAAATCA 913  
 QY 841 TTGGGATTTTATTCACAGTTTATTAATATACAGTCACTTTTCAAAAAATTTGGATTTT 900  
 DB 914 TTGGGATTTTATTCACAGTTTATTAATATACAGTCACTTTTCAAAAAATTTGGATTTT 973  
 QY 901 TTTATATATTAACCTAGCTGCTATTCAAATGTGAGTCTACCAATTTTATTTATGTTCAAC 960  
 DB 974 TTTATATATTAACCTAGCTGCTATTCAAATGTGAGTCTACCAATTTTATTTATGTTCAAC 1033  
 QY 961 TGTTTGTGAGACTGAATTC 979  
 DB 1034 TGTTTGTGAGACTGAATTC 1052  
 RESULT 6  
 ID ABX63609 standard; cDNA, 2540 BP.  
 XX ABX63609;  
 AC  
 XX  
 DT 26-FEB-2003 (first entry)  
 XX  
 DE Human cDNA #609 differentially expressed in activated vascular tissue.  
 XX  
 KW Human; gene; ss; vascular tissue; cytosolic; atherosclerosis; cardiac;  
 KW hypotensive; antidiabetic; gynaecological; vasotrophic; cerebroprotective;  
 KW gene therapy; vascular disease; cancer; coronary; artery disease;  
 KW hypertension; diabetes; pre-eclampsia; restenosis;  
 KW ischaemia-reperfusion injury; stroke.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2002137081-A1.  
 XX

PD 26-SEP-2002.  
 XX  
 XX 08-JAN-2002; 2002US-00044090.  
 XX  
 XX 28-JUL-2000; 2000US-0222469P.  
 PR 08-JAN-2001; 2001US-0260483P.  
 XX  
 PA (BAND/) BANDMAN O.  
 XX  
 XX Bandman O;  
 PI  
 DR WPI, 2003-110597/10.  
 XX  
 XX  
 PT Combination for diagnosing, staging, treating, or monitoring the  
 PT progression of treatment of a vascular disease, e.g. atherosclerosis,  
 PT comprises several cDNAs that are differentially expressed in activated  
 PT vascular tissue.  
 PR  
 XX  
 XX Claim 1, Page: 18pp, English.  
 PS  
 PS This invention relates to a combination comprising several cDNAs that are  
 CC differentially expressed in activated vascular tissue. The invention also  
 CC discloses a high throughput method for detecting differentially expressed  
 CC cDNAs in a sample. The cDNAs of the invention may have  
 CC antiarteriosclerotic; cytosolic; cardiac; hypotensive; antidiabetic;  
 CC gynaecological; vasotrophic and cerebroprotective activities and may be  
 CC used in gene therapy. The cDNAs of the invention may be used in a high-  
 CC throughput methods for detecting differential expression of one or more  
 CC cDNAs in a sample, or screening several molecules or compounds to  
 CC identify a molecule or compound that specifically binds a cDNA of the  
 CC invention. A protein encoded by the cDNA may be used to screen several  
 CC molecules or compounds to identify a ligand that specifically binds to  
 CC the protein, or to produce or purify an antibody to the protein that can  
 CC be used to detect a protein in a sample or purify a natural or  
 CC recombinant protein from a sample. The nucleotides may be useful for  
 CC diagnosing, staging, treating or monitoring the progression of treatment  
 CC of a vascular disease, e.g. atherosclerosis, cancer, coronary artery  
 CC disease, hypertension, diabetes, pre-eclampsia, ischaemia-reperfusion  
 CC injury, restenosis, or stroke. The cDNAs can also be used for large-scale  
 CC genetic or gene expression analysis of several new nucleic acid  
 CC molecules. Antibodies to the proteins encoded by the cDNAs are useful for  
 CC diagnosing pre-pathologic disorders, and chronic or acute diseases  
 CC associated with abnormalities in the expression, amount or distribution  
 CC of the protein. The present sequence represents a cDNA of the invention  
 CC that is differentially expressed in activated vascular tissue. Note: The  
 CC sequence data for this patent did not form part of the specification, but  
 CC was obtained in electronic format directly from USPTO at  
 CC <http://seqdata.uspto.gov/sequence.html?docid=20020137081>  
 XX  
 SQ Sequence 2540 BP; 806 A; 458 C; 534 G; 742 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 979; DB 8; Length 2540;  
 Best Local Similarity 100.0%; Pred. No. 26-257;  
 Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAAGCGCTTGGCCAGCGGCGCCGACCCCTGACACCAAGAACCCCGCTGCCCTTGG 60  
 DB 27 GGAAGCGCTTGGCCAGCGGCGCCGACCCCTGACACCAAGAACCCCGCTGCCCTTGG 86  
 QY 61 GGCTGTGATTTCTGCTCTTTTCTTGAACGAGGCTGCACTGGGGGAGTCTCAAGAGC 120  
 DB 87 GGCTGTGATTTCTGCTCTTTTCTTGAACGAGGCTGCACTGGGGGAGTCTCAAGAGC 146  
 QY 121 CAACAGAAATTAACGCGAGATCTGTCTCTGACCCCTAGACTAGAGAACCTGCGCGGCC 180  
 DB 147 CAACAGAAATTAACGCGAGATCTGTCTCTGACCCCTAGACTAGAGAACCTGCGCGGCC 206  
 QY 181 TACTTCTCCGTACTACTAGACAGTACAGCAAGCTGCGCGCAAGTCTGTACGGGG 240  
 DB 207 TACTTCTCCGTACTACTAGACAGTACAGCAAGCTGCGCGCAAGTCTGTACGGGG 266  
 QY 241 GCTGGAGGCGCAACCAATTTCTACCTTGGAGGCTTGTGAGAGTCTTGTGGA 300

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Db      267 GCTGCGAGGGCAACGCCAACATTTCTACACCTGGAGGGCTTGACAGCATGCTTGCTGGA 326
Qy      301 GATGAGAAAAAGTTTCCCAAAAGTTTCCGGCTGCAAGTGAAGTGGACCAACGATGAGG 360
Db      327 GATGAGAAAAAGTTTCCCAAAAGTTTCCGGCTGCAAGTGAAGTGGACCAACGATGAGG 386
Qy      361 GGTCCACAGAAAAGTATTTCTTAATCTTAAGTTCAGTGCATGATGAAAAATCTTTTCG 420
Db      387 GGTCCACAGAAAAGTATTTCTTAATCTTAAGTTCAGTGCATGATGAAAAATCTTTTCG 446
Qy      421 GTGGGTGTCAACCGGAACCGGATGGAACAGGTTTCCAGATGACCTAATTGTATGGGCT 480
Db      447 GTGGGTGTCAACCGGAACCGGATGGAACAGGTTTCCAGATGACCTAATTGTATGGGCT 506
Qy      481 TCTGGGCAACCAAGAAATTTCCATCATTTTGTCTACAGTCCAAAAGATGAGGACCTGTGCT 540
Db      507 TCTGGGCAACCAAGAAATTTCCATCATTTTGTCTACAGTCCAAAAGATGAGGACCTGTGCT 566
Qy      541 CTGCAATGTGATCGCTATTTATTTAATCCAAAGATACAGAACTGTGATGCTTCACT 600
Db      567 CTGCAATGTGATCGCTATTTATTTAATCCAAAGATACAGAACTGTGATGCTTCACT 626
Qy      601 ATACTGGCTGTGAGGAGGAAATGCAATTAATTTGTTAGCAGGAGGATTCGCAACGTCAT 660
Db      627 ATACTGGCTGTGAGGAGGAAATGCAATTAATTTGTTAGCAGGAGGATTCGCAACGTCAT 686
Qy      661 GTGCAAAAAGCTTTGAAAAAGAAAAAGAAATGCCAAAGCTTTGCTTGGCAGTAAATCC 720
Db      687 GTGCAAAAAGCTTTGAAAAAGAAAAAGAAATGCCAAAGCTTTGCTTGGCAGTAAATCC 746
Qy      721 GGAANAATCGGAAGAGCAATTTTAAACATCTTAAATATGTCATCTGTTGCTTTATG 780
Db      747 GGAANAATCGGAAGAGCAATTTTAAACATCTTAAATATGTCATCTGTTGCTTTATG 806
Qy      781 GCTATTTGCTTTATGTTGTTATCTGAAGATTAATATGACAGCATGAGAAAACAATCA 840
Db      807 GCTATTTGCTTTATGTTGTTATCTGAAGATTAATATGACAGCATGAGAAAACAATCA 866
Qy      841 TTGGTGATTTATTCACAGTTTATTTAATATACAGTCACTTTTCAAAAATTTGATTTT 900
Db      867 TTGGTGATTTATTCACAGTTTATTTAATATACAGTCACTTTTCAAAAATTTGATTTT 926
Qy      901 TTTATATATTAATTAAGTCTATTTCAAAATGATGATCACTTTTAAATTTATGTTCAAC 960
Db      927 TTTATATATTAATTAAGTCTATTTCAAAATGATGATCACTTTTAAATTTATGTTCAAC 986
Qy      961 TGTGTTGTGAGACTGAATTC 979
Db      987 TGTGTTGTGAGACTGAATTC 1005

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RESULT 7  
ID ADJ56337 standard; cDNA; 2540 BP.

AC ADJ56337;  
DT 06-MAY-2004 (first entry)  
DE Human cDNA differentially expressed in MYCN activated cells Segid 143.  
XX human, differential expression; transactivator; proto-oncogene;  
KM neuroblastoma; small cell lung cancer; cytotoxic; gene therapy; ss;  
XX MYCN activated cell.  
OS Homo sapiens.  
XX  
XX US2003119009-A1.  
XX 26-JUN-2003.  
XX  
XX 25-FEB-2002; 2002US-00084817.  
XX

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PR      23-FEB-2001; 2001US-0270784P.
XX
XX (STUA/) STUART S G.
PA (NUCH/) NUCHTERN J G.
PA (PION/) PION S B.
PA (SHOH/) SHOHER J M.
XX
XX Stuart SG, Nuchtern JG, Pion SB, Shoher JM;
XX WPI: 2003-635698/60.
XX
XX New genes regulated by MYCN activation, useful in gene therapy,
XX particularly for treating a subject with e.g. neuroblastoma or other
XX cancers, or for diagnosing, staging or monitoring the treatment of the
XX cancer.
XX
XX Claim 1; SEQ ID NO 143; 27bp; English.
XX
XX This invention relates to novel isolated cDNAs that are differentially
XX expressed in MYCN activated cells. Specifically, it refers to
XX polynucleotide sequences that exhibit differential expression patterns in
XX cells activated by the transactivator MYCN, where MYCN is a proto-
XX oncogene that is amplified in neuroblastoma cells and is common in small
XX cell lung cancers. The present invention describes these cDNA molecules
XX as useful for in hybridisation assays to detect expression of nucleic
XX acids (or complementary nucleic acids) in a present in a given sample, as
XX well as for screening assays by identifying molecules or compounds that
XX specifically bind the cDNA as a ligand and modulate function or activity.
XX Accordingly, these compositions exhibit cytotoxic activity and can also
XX be used for gene therapy purposes. This polynucleotide sequence is a cDNA
XX that is differentially expressed in MYCN activated cells, given in an
XX exemplification of the invention. NOTE: This sequence does not appear in
XX the printed specification but has been obtained in electronic format from
XX the US Patent Office at
XX ftp://seqdata.uspto.gov/sequence.html?docid=20030119009.
XX
XX Sequence 2540 BP; 806 A; 458 C; 534 G; 742 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 979; DB 10; Length 2540;
XX Best Local Similarity 100.0%; Pred. No. 2e-257;
XX Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GAGAGCCCTTGGCCACGCGGCGCGCCGACCCCTGACACATGGAACCCGCTGCGCCCTGG 60
XX 27 GAGAGCCCTTGGCCACGCGGCGCGCCGACCCCTGACACATGGAACCCGCTGCGCCCTGG 86
XX
XX 61 GGCTGTGATTTCTGCTCTTTTCTGACGAGGCTGCACTGGGCGATGCTGCTCAGAGC 120
XX 87 GGCTGTGATTTCTGCTCTTTTCTGACGAGGCTGCACTGGGCGATGCTGCTCAGAGC 146
XX
XX 121 CAACAGAAATTAAGCGGGAATGTGTCTCTGCGCCCTGACTAGCAACCTTCCGGGCCC 180
XX 147 CAACAGAAATTAAGCGGGAATGTGTCTCTGCGCCCTGACTAGCAACCTTCCGGGCCC 206
XX
XX 181 TACTTCTCGTTACTACTACGACAGGTACGACAGAGCTGCGCGAGTTCTGTACGGGG 240
XX 207 TACTTCTCGTTACTACTACGACAGGTACGACAGAGCTGCGCGAGTTCTGTACGGGG 266
XX
XX 241 GCTGCGAGGGCAACGCCCAATTTCTACACCTGGAGGCTTTCGACGATGCTTCTGGA 300
XX 267 GCTGCGAGGGCAACGCCCAATTTCTACACCTGGAGGCTTTCGACGATGCTTCTGGA 326
XX
XX 301 GATGAGAAAAAGTTTCCCAAAAGTTTCCGGCTGCAAGTGAAGTGGACCAACGATGAGG 360
XX 327 GATGAGAAAAAGTTTCCCAAAAGTTTCCGGCTGCAAGTGAAGTGGACCAACGATGAGG 386
XX
XX 361 GGTCCACAGAAAAGTATTTCTTAATCTTAAGTTCAGTGCATGATGAAAAATCTTTTCG 420
XX 387 GGTCCACAGAAAAGTATTTCTTAATCTTAAGTTCAGTGCATGATGAAAAATCTTTTCG 446
XX
XX 421 GTGGGTGTCAACCGGAACCGGATGGAACAGGTTTCCAGATGACCTAATTGTATGGGCT 480
XX 447 GTGGGTGTCAACCGGAACCGGATGGAACAGGTTTCCAGATGACCTAATTGTATGGGCT 506

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QY 481 TCTGGCACCAGAAATTCATCTTTTCTACGTCGCAAAAGATGAGGAGCTGTGCT 540  
 DB 507 TCTGGCACCAGAAATTCATCTTTTCTACGTCGCAAAAGATGAGGAGCTGTGCT 566  
 QY 541 CTGCCAATGTGACTGCTATTTATTTATTCAGAGATGAGAACTGTGATGCTTCACT 600  
 DB 567 CTGCCAATGTGACTGCTATTTATTTATTCAGAGATGAGAACTGTGATGCTTCACT 626  
 QY 601 AATCTGCTGTGAGGAGATGACAAATTAATTTATGAGGAGATTCGCAACGTGAT 660  
 DB 627 AATCTGCTGTGAGGAGATGACAAATTAATTTATGAGGAGATTCGCAACGTGAT 686  
 QY 661 GTGCCAATGTGAGGAGATGAGAAATGAGATGAGGAGATTCGCAACGTGAT 720  
 DB 687 GTGCCAATGTGAGGAGATGAGAAATGAGATGAGGAGATTCGCAACGTGAT 746  
 QY 721 GGAATATTTGGAAGAGATTTTAAACATTTCTTAATATGATGCTGTGCTTATG 780  
 DB 747 GGAATATTTGGAAGAGATTTTAAACATTTCTTAATATGATGCTGTGCTTATG 806  
 QY 781 GCTTATTTGCTTATGTTGTTATCTGAAGAAATATATGACATGAGAAACAAATCA 840  
 DB 807 GCTTATTTGCTTATGTTGTTATCTGAAGAAATATATGACATGAGAAACAAATCA 866  
 QY 841 TTGGTGATTTATTCACAGTTTATTTATTAATCAAGTCACTTTTCAAAATTTGATTT 900  
 DB 867 TTGGTGATTTATTCACAGTTTATTTATTAATCAAGTCACTTTTCAAAATTTGATTT 926  
 QY 901 TTTATATATTAATTAATGCTATTTCAAAATGAGTCAATTTTATTAATTTATGTTCAAC 960  
 DB 927 TTTATATATTAATTAATGCTATTTCAAAATGAGTCAATTTTATTAATTTATGTTCAAC 986  
 QY 961 TGTGTGTGAGACTGAATTC 979  
 DB 987 TGTGTGTGAGACTGAATTC 1005

RESULT 8  
 ID ADS19178 standard; cDNA, 1141 BP.  
 AC ADS19178;  
 XX 16-DEC-2004 (first entry)  
 DT Human tissue factor pathway inhibitor 2 cDNA, SEQ ID NO:19.  
 DE Human tissue factor pathway inhibitor 2 cDNA, SEQ ID NO:19.  
 XX Mesenchymal stem cell; marker gene; serine protease inhibitor;  
 KM cytosolic protease inhibitor; adrenomedullin; apolipoprotein D;  
 KM collagen type XV alpha 1; CUG triplet repeat RNA binding protein;  
 KM dermatopontin; isocitrate dehydrogenase 2;  
 KM major histocompatibility complex class II; MHC class II; DR beta 3;  
 KM DR alpha; protein tyrosine kinase 7; Sam68-like phosphotyrosine protein;  
 KM C-type lectin superfamily member 2; matrix metalloproteinase 1;  
 KM tissue factor pathway inhibitor 2; microarray; DNA chip; detection;  
 KM identification; human; ss.  
 XX Homo sapiens.  
 OS MO2004081174-A2.  
 PN 23-SEP-2004.  
 PD 27-FEB-2004; 2004MO-JP002457.  
 PF 10-MAR-2003; 2003JP-00063077.  
 PR (MISC-) JAPAN SCI & TECHNOLOGY AGENCY.  
 PA (TWO-) TWO CELLS CO LTD.  
 PA (KATO/) KATO Y.  
 XX Kato Y, Tsuji K, Koike C;  
 PI

XX WPI: 2004-699450/68.  
 DR GENBANK; AL550357.  
 DB New gene markers e.g. serine or cysteine protease inhibitor gene, major  
 PT histocompatibility complex class II gene specific for mesenchymal stem  
 PT cells, useful for detecting and identifying mesenchymal stem cells.  
 XX Claim 1; SEQ ID NO 19; 171bp; Japanese.  
 PS  
 CC The invention relates to marker genes for detecting mesenchymal stem  
 CC cells, selected from approximately 145 genes. The mesenchymal stem cell  
 CC marker genes include the serine (or cysteine) protease inhibitor gene  
 CC (ADS19160), the adrenomedullin gene (ADS19161), the apolipoprotein D gene  
 CC (ADS19163), the collagen type XV alpha 1 gene (ADS19165), the CUG triplet  
 CC repeat RNA binding protein 2 gene (ADS19166), the dermatopontin gene  
 CC (ADS19168), the isocitrate dehydrogenase 2 gene (ADS19169), the major  
 CC histocompatibility complex class II DR beta 3 or DR alpha genes (ADS19170  
 CC and ADS19205, respectively), the protein tyrosine kinase 7 gene  
 CC (ADS19171), the Sam68-like phosphotyrosine protein (ADS19173), the C-type  
 CC lectin superfamily member 2 gene (ADS19174), the matrix metalloproteinase 1  
 CC gene (ADS19176), and the tissue factor pathway inhibitor 2 gene  
 CC (ADS19178). The invention also relates to marker gene-specific probes and  
 CC microarrays or DNA chips comprising such probes; reverse transcription-  
 CC PCR (RT-PCR) and real-time PCR primers specific for marker genes of the  
 CC invention (ADS19179-ADS19204 and ADS19206-ADS19275); mesenchymal stem  
 CC cell polypeptide markers (ADS19162, ADS19164, ADS19167, ADS19172,  
 CC ADS19175 and ADS19177) and antibodies specific for them; and kits  
 CC comprising probe microarrays or antibodies for identifying mesenchymal  
 CC stem cells. The marker genes and polypeptides, probe microarrays, primers  
 CC and antibodies permit easy and reliable detection and identification of  
 CC mesenchymal stem cells, e.g., by determining the expression level of a  
 CC marker gene and subsequently performing Northern blot analysis. The  
 CC present sequence represents a specifically claimed human tissue factor  
 CC pathway inhibitor 2 cDNA.  
 XX  
 SQ Sequence 1141 BP; 317 A; 246 C; 259 G; 319 T; 0 U; 0 Other;  
 Query Match 99.8%; Score 977.4; DB 13; Length 1141;  
 Best Local Similarity 99.9%; Pred. No. 3.7e-257;  
 Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GGAGCGCTTGGCCAGCGGCGCGCCGACCCCTGACACATGAGACCCCGCTGCCCTTGG 60  
 DB 18 GGAGCGCTTGGCCAGCGGCGCGCCGACCCCTGACACATGAGACCCCGCTGCCCTTGG 77  
 QY 61 GGCTGTGATTTCTGCTGCTTTTCTGACGAGGCTGCACTGGGCGATGCTCTGACGAGC 120  
 DB 78 GGCTGTGATTTCTGCTGCTTTTCTGACGAGGCTGCACTGGGCGATGCTCTGACGAGC 137  
 QY 121 CAACAGGAATTAACGCGGAGATGTCCTCTGCCCCCTAGACTAGAGACCTGCGGGGCC 180  
 DB 138 CAACAGGAATTAACGCGGAGATGTCCTCTGCCCCCTAGACTAGAGACCTGCGGGGCC 197  
 QY 181 TACTTCTCCGTTACTACTACAGACGATACGACGAGTGCCTGCTTCTGTAACGGGG 240  
 DB 198 TACTTCTCCGTTACTACTACAGACGATACGACGAGTGCCTGCTTCTGTAACGGGG 257  
 QY 241 GCTGCGAGGGCAACGCAATTTCTACCTGAGGAGCTTGGAGAGATGCTTCTGTAACGGGG 300  
 DB 258 GCTGCGAGGGCAACGCAATTTCTACCTGAGGAGCTTGGAGAGATGCTTCTGTAACGGGG 317  
 QY 301 GGATGAAAAAGTTCCCAAGTTTCCGGCTGCAAGTGAAGTGAAGCAACAGTGTGAGG 360  
 DB 318 GGATGAAAAAGTTCCCAAGTTTCCGGCTGCAAGTGAAGTGAAGCAACAGTGTGAGG 377  
 QY 361 GGTCCAGAAAAATATTTCTTTATCTTAAGTTCATGACATGTGAAAAATTTCTTTTCCG 420  
 DB 378 GGTCCAGAAAAATATTTCTTTATCTTAAGTTCATGACATGTGAAAAATTTCTTTTCCG 437  
 QY 421 GTGGGTGACCCGGAACCGGATTGAGAAACAGGTTTCCAGATGAGCTACTGTATGAGGCT 480  
 DB 438 GTGGGTGACCCGGAACCGGATTGAGAAACAGGTTTCCAGATGAGCTACTGTATGAGGCT 497

QY 481 TCTGGCACAAGAAATTCATCTTGTCTAGTCCAAAAGATGAGGACCTGCT 540  
DB 498 TCTGGCACAAGAAATTCATCTTGTCTAGTCCAAAAGATGAGGACCTGCT 557  
QY 541 CTGCAATGTGACCTGCTATTATTTAAATCCAAAGATGAGGACCTGCTGCT 600  
DB 558 CTGCAATGTGACCTGCTATTATTTAAATCCAAAGATGAGGACCTGCTGCT 617  
QY 601 ATACTGCTGTGAGGAGAAATGCAATTAATCTTTAGCAGGAGATTCGAAACCTGAT 660  
DB 618 ATACTGCTGTGAGGAGAAATGCAATTAATCTTTAGCAGGAGATTCGAAACCTGAT 677  
QY 661 GTGCAAAAGCTTTGAAAAAGAAAGAGAGCCAAAGCTTCCCTTCCAGTAAATCC 720  
DB 678 GTGCAAAAGCTTTGAAAAAGAAAGAGAGCCAAAGCTTCCCTTCCAGTAAATCC 737  
QY 721 GGAATATTCGAAAGAAATTTAAATCTTAATATGATCTGTTGCTTTTANG 780  
DB 738 GGAATATTCGAAAGAAATTTAAATCTTAATATGATCTGTTGCTTTTANG 797  
QY 781 GCTTATTTGCTTTATGTTGTTATGTAAGAAATTAATGACAGATGAGAAACAAATCA 840  
DB 798 GCTTATTTGCTTTATGTTGTTATGTAAGAAATTAATGACAGATGAGAAACAAATCA 857  
QY 841 TTGGTGATTTATTCACCACTTTTATTAATACAGTCACTTTTCAAAAATTTGATTT 900  
DB 858 TTGGTGATTTATTCACCACTTTTATTAATACAGTCACTTTTCAAAAATTTGATTT 917  
QY 901 TTATATATTAATCTAGCTGCTATTAATGATGAGTCACTTTTAAATTAATGTTCAAC 960  
DB 918 TTATATATTAATCTAGCTGCTATTAATGATGAGTCACTTTTAAATTAATGTTCAAC 977  
QY 961 TGTGTTGAGACTGAATTC 979  
DB 978 TGTGTTGAGACTGAATTC 996

## RESULT 9

AB876528 standard; cDNA, 1142 BP.

AB876528;

11-DEC-2002 (first entry)

CDNA encoding human ovarian cancer marker M588.

Human, ovarian cancer, marker; cancer; familial history; brain disorder; central nervous system disorder; bacterial meningitis; viral meningitis; Alzheimer's disease; Parkinson's disease; cerebral edema; hydrocephalus; brain herniation; inflammation; encephalitis; testicular disorder; non-tuberculous granulomatous orchitis; connective tissue disorder; heart disorder; ischemic heart disease; atherosclerosis; neoplasm; histological type: carcinogenic; ovarian cancer marker; gene; se.

Homo sapiens.

MO200271928-A2.

19-SEP-2002.

14-MAR-2002; 2002WO-US007826.

14-MAR-2001; 2001US-0276025P.

14-MAR-2001; 2001US-0276026P.

10-AUG-2001; 2001US-0311732P.

19-SEP-2001; 2001US-0323580P.

26-SEP-2001; 2001US-0324967P.

26-SEP-2001; 2001US-0325102P.

26-SEP-2001; 2001US-0325149P.

(MILL-) MILLENNIUM PHARM INC.

Monahan JR, Gannavarapu M, Hoersch S, Kamath S, Kovatis SG; Meyers RE, Morrissey MP, Olandt PJ, Sen A, Vleehy FO, Mills GB; Baer RC, Lu K, Schmandt RE, Zhao X, Glatt K; WPI, 2002-723277/78. P-Psdb; ABG96429.

Assessing whether a patient is afflicted with ovarian cancer, useful in assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and from a non cancer patient.

Disclosure: Page 437; 481pp; English.

The present invention relates to a new method for assessing whether a patient is afflicted with ovarian cancer. The method involves comparing the expression level of a marker in a patient sample and the normal level of expression of the marker in a control non-ovarian cancer sample, where the marker is selected from 363 cancer markers described in the specification. The method of the invention is useful in diagnosing or characterizing cancer, in detecting the presence of cancer as early as possible, and the recurrence of ovarian cancer. The method may also be of particular use with patients having an enhanced risk of developing ovarian cancer (e.g. patients having a familial history of ovarian cancer). The cancer markers may be used in the management and treatment of e.g. brain and central nervous system disorders (e.g. bacterial and viral meningitis, Alzheimer's disease or Parkinson's disease), brain disorders (e.g. cerebral edema, hydrocephalus or brain herniations), inflammations (e.g. bacterial or viral meningitis or encephalitis), testicular disorders (e.g. non-tuberculous granulomatous orchitis), connective tissue disorders, or heart disorders (e.g. ischaemic heart disease or atherosclerosis). The compositions and methods may also be used in assessing the histological type of neoplasm associated with ovarian cancer, monitoring the progression of ovarian cancer, determining whether ovarian cancer has metastasized or is likely to metastasize, selecting a composition for inhibiting ovarian cancer, assessing the ovarian carcinogenic potential of a compound, or inhibiting ovarian cancer or at risk of developing ovarian cancer. The present nucleic acid sequence encodes one of the ovarian cancer markers described in the invention.

Sequence 1142 BP; 316 A; 248 C; 260 G; 318 T; 0 U; 0 Other;

Query Match 99.3%; Score 972.2; DB 6; Length 1142;

Best Local Similarity 99.7%; Pred. No. 9.9e-256; Matches 974; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAAGCCTTGGCCAGCGGGGCGCCGACCCCTGACAGATGAGACCCGCTGCGCCCGG 60  
DB 19 GAGCGCCTTGGCCAGCGGGGCGCCGACCCCTGACAGATGAGACCCGCTGCGCCCG 78  
QY 61 GAGCTGCAATCTGCTGCTTTTCCGAGGAGCTGCACTGCGGAGATCTGCTGAGAGC 120  
DB 79 GAGCTGCAATCTGCTGCTTTTCCGAGGAGCTGCACTGCGGAGATCTGCTGAGAGC 138  
QY 121 CAACAGAAATPACGCGGAGATCTGCTGCTGCTGCTGACCTGACCTGCGGCGCC 180  
DB 139 CAACAGAAATPACGCGGAGATCTGCTGCTGCTGCTGACCTGACCTGCGGCGCC 198  
QY 181 TACTTCTCGTTACTACACAGATGAGTACAGGAGTGGCGGAGTTCCTGTAAGGAGG 240  
DB 199 TACTTCTCGTTACTACACAGATGAGTACAGGAGTGGCGGAGTTCCTGTAAGGAGG 258  
QY 241 GCTGCGAGGCAAGCCCAATTTCTTCACTGCGAGGCTTTCGACAGATCTTCTGGA 300  
DB 259 GCTGCGAGGCAAGCCCAATTTCTTCACTGCGAGGCTTTCGACAGATCTTCTGGA 318  
QY 301 GGAATGAAAAAGTTCCAAAGTTTCCGCGCTGCAAGTGAAGTGAACAAGTGTGAGG 360  
DB 319 GGAATGAAAAAGTTCCAAAGTTTCCGCGCTGCAAGTGAAGTGAACAAGTGTGAGG 378  
QY 361 GGTCCAGAGAAAGATTTCTTTAATCTAAGTTCATGACATGAGAAATTTCTTTCCG 420



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Db 379 GGTCCACGAAAAAGTATTCCTTAATCTAAGTTCATGACATGTAATAATTCCTTTCG 438
Qy 421 GTGGGTGTCAACCGGAACCGATTTGAGAACAGGTTTCCAGATGAAGCTACTGTATGGCT 480
Db 439 GTGGGTGTCAACCGGAACCGATTTGAGAACAGGTTTCCAGATGAAGCTACTGTATGGCT 498
Qy 481 TCTGCGCACCAAGAAAATTCATCATTTTGTCTACAGTCCAAAGATGAGGAGCTGTGCT 540
Db 499 TCTGCGCACCAAGAAAATTCATCATTTTGTCTACAGTCCAAAGATGAGGAGCTGTGCT 558
Qy 541 CTGCGCAATGTAGCTGCTATTAATTTAATCCAGATGAGGAGCTGTATGCTTCACT 600
Db 559 CTGCGCAATGTAGCTGCTATTAATTTAATCCAGATGAGGAGCTGTATGCTTCACT 618
Qy 601 ATACTGCTGTGAGGAGATGACAAATTAATCTTGTAGGAGGAGATGCAAACTGTGAT 660
Db 619 ATACTGCTGTGAGGAGATGACAAATTAATCTTGTAGGAGGAGATGCAAACTGTGAT 678
Qy 661 GTGCAAAAGCTTTGAAAAAGAAAAGAAAGATGCCAAAGCTTGTGCTTGCAGTAGAATCC 720
Db 679 GTGCAAAAGCTTTGAAAAAGAAAAGAAAGATGCCAAAGCTTGTGCTTGCAGTAGAATCC 738
Qy 721 GGAATATTCGAAAGAGCAATTTTAACATCTTAAATATGTCATCTTGTGTCTTTATG 780
Db 739 GGAATATTCGAAAGAGCAATTTTAACATCTTAAATATGTCATCTTGTGTCTTTATG 798
Qy 781 GCTATTTGCTTTTGTGTGTATCTGAAGATTAATATGACAGATGAGAGAAACAATCA 840
Db 799 GCTATTTGCTTTTGTGTGTATCTGAAGATTAATATGACAGATGAGAGAAACAATCA 858
Qy 841 TTGGTGAATTAATCAACAGTTTAAATTAATACAGTCACTTTTCAAAAATTTGGATTTT 900
Db 859 TTGGTGAATTAATCAACAGTTTAAATTAATACAGTCACTTTTCAAAAATTTGGATTTT 918
Qy 901 TTTAATATTAATCACTGCTATCTCAATGATGATGATCACTTTTAATTAATGTTTCAAC 960
Db 919 TTTAATATTAATCACTGCTATCTCAATGATGATGATCACTTTTAATTAATGTTTCAAC 978
Qy 961 TGTGTGTGAGACTGAAT 977
Db 979 TGTGTGTGAGACTGAAT 995

RESULT 10
ABX76328
ID ABX76328 standard; DNA; 1142 BP.
AC ABX76328;
XX
DX 02-APR-2003 (first entry)
DE
XX Lung cancer-associated polynucleotide #192.
XX
XX Lung cancer-associated polynucleotide; gene; de; cytostatic; emphysema;
XX antiinflammatory; antiaesthetic; non-small cell lung cancer; atelectasis;
XX small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
XX chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
XX interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
XX Unidentified.
OS
XX
XX WO200286443-A2.
XX
XX 31-OCT-2002.
XX
XX 18-APR-2002; 2002WO-US012476.
XX
XX 18-APR-2001; 2001US-0284770P.
XX 10-MAY-2001; 2001US-0290492P.
XX 09-NOV-2001; 2001US-0339245P.
XX 13-NOV-2001; 2001US-0350666P.
XX 29-NOV-2001; 2001US-0334370P.
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PR 12-APR-2002; 2002US-0372246P.
XX
XX (BOSB-) BOS BIOTECHNOLOGY INC.
XX
XX Aziz N, Murray R;
XX WPI; 2003-093161/08.
DR P-PSDB; ABUS65599.
XX
XX Detecting a lung cancer-associated transcript in a cell from a patient
XX for treating lung cancer, by contacting a biological sample from the
XX patient with a polynucleotide that exhibits increased or decreased
XX expression in lung cancer.
XX
XX Claim 22; Page 332-333; 453pp; English.
XX
XX The invention relates to a method for detecting a lung cancer-associated
XX transcript in a cell from a patient, comprising contacting a biological
XX sample from the patient with a polynucleotide that selectively hybridizes
XX to a sequence that is at least 80 % identical to a gene that exhibits
XX increased or decreased expression in lung cancer samples. Lung cancer-
XX associated polynucleotides and polypeptides are used for identifying a
XX compound that modulates a lung cancer-associated polypeptide, for
XX inhibiting proliferation of a lung cancer-associated cell to treat lung
XX cancer in a patient and for treating a mammal having lung cancer by
XX administering a modulatory compound identified. The methods are useful
XX for treating lung cancer, such as small cell lung cancer, non-small cell
XX lung cancer or other benign or precancerous lesions, e.g. atelectasis,
XX emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
XX hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma, and
XX bronchiectasis. The genes, polynucleotides and polypeptides are useful
XX for diagnostic purposes and as targets for screening for therapeutic
XX compounds that modulate lung cancer, such as antibodies. Sequences
XX ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
XX invention.
XX
XX Sequence 1142 BP; 316 A; 248 C; 260 G; 318 T; 0 U; 0 Other;
SQ
XX
XX Query Match 99.3%; Score 972.2; DB 8; Length 1142;
XX Best Local Similarity 99.7%; Pred. No. 9.9e-256;
XX Matches 974; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 GGACGCTTGGCCAGCGGCGCCGACCCCTTGACACATGAGACCCGCTGCCCCCTGG 60
Db 19 GGACGCTTGGCCAGCGGCGCCGACCCCTTGACACATGAGACCCGCTGCCCCCTGG 78
Qy 61 GGCTGTGATTCCTGCTGTTTCTGACGAGGCTGACCTGCGGAGATCTGTACAGAGC 120
Db 79 GGCTGTGATTCCTGCTGTTTCTGACGAGGCTGACCTGCGGAGATCTGTACAGAGC 138
Qy 121 CAACAGAAATTAACGCGAGATCTGTCTCTGCCCCCTAGACTAGAGACCTGCGGAGCC 180
Db 139 CAACAGAAATTAACGCGAGATCTGTCTCTGCCCCCTAGACTAGAGACCTGCGGAGCC 198
Qy 181 TACTTTCCTGTTACTTACTACAGACAGTACACGAGAGCTGCGGCAATCTGTACAGGG 240
Db 199 TACTTTCCTGTTACTTACTACAGACAGTACACGAGAGCTGCGGCAATCTGTACAGGG 258
Qy 241 GCTGCGAGGGCAAGCAATTTCTACACTCTGAGAGGCTTGTGAGAGAGCTTGTCTGGA 300
Db 259 GCTGCGAGGGCAAGCAATTTCTACACTCTGAGAGGCTTGTGAGAGAGCTTGTCTGGA 318
Qy 301 GGATAGAAAAAGTCCCAAGTTTCCGCGCTGCAAGTGTGAGAGCAACAGTGTAGG 360
Db 319 GGATAGAAAAAGTCCCAAGTTTCCGCGCTGCAAGTGTGAGAGCAACAGTGTAGG 378
Qy 361 GGTCCACGAAAGATTTCTTATATCTAAGTTCATGACATGTGAAAAATTTCTTTTCCG 420
Db 379 GGTCCACGAAAGATTTCTTATATCTAAGTTCATGACATGTGAAAAATTTCTTTTCCG 438
Qy 421 GTGGGTGTCAACCGGAACCGATTTGAGAACAGGTTTCCAGATGAAGCTACTGTATGGCT 480
Db 439 GTGGGTGTCAACCGGAACCGATTTGAGAACAGGTTTCCAGATGAAGCTACTGTATGGCT 498
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OY 481 TCTGGCCACCAAGAAATTCATCTTGTCTACAGTCCAAAAGATGAGGGACGTGTCT 540
DB 499 TCTGGCCACCAAGAAATTCATCTTGTCTACAGTCCAAAAGATGAGGGACGTGTCT 558
OY 541 CTGCCAATGTGACTGCTATTTATTTAATCCAAAGATGAGAACTGTGTCTTCACT 600
DB 559 CTGCCAATGTGACTGCTATTTATTTAATCCAAAGATGAGAACTGTGTCTTCACT 618
OY 601 ATACTGCTGTGAGGAGAAATGACATTAATCTTGTAGCAGGAGATTCGAAACGTGCAT 660
DB 619 ATACTGCTGTGAGGAGAAATGACATTAATCTTGTAGCAGGAGATTCGAAACGTGCAT 678
OY 661 GTGCAAAAGCTTTGAAAAAGAAAAAGATGAGAAAGATTCGCTTGCAGTAAATCC 720
DB 679 GTGCAAAAGCTTTGAAAAAGAAAAAGATGAGAAAGATTCGCTTGCAGTAAATCC 738
OY 721 GGAATATTCGAAAGAGCAATTTTAAACATCTTAATATGTCATCTGTGTCTTTATG 780
DB 739 GGAATATTCGAAAGAGCAATTTTAAACATCTTAATATGTCATCTGTGTCTTTATG 798
OY 781 GCTTATTTGCTTTATGTTGTATCTGAAGATTAATATGACGATGAGAAACAAATCA 840
DB 799 GCTTATTTGCTTTATGTTGTATCTGAAGATTAATATGACGATGAGAAACAAATCA 858
OY 841 TTGCGATTTATTCACCAAGTTTATTAATACAGTCACTTTTCAAAAATTTGATTTT 900
DB 859 TTGCGATTTATTCACCAAGTTTATTAATACAGTCACTTTTCAAAAATTTGATTTT 918
OY 901 TTTATATATTAACCTAGCTGCTATTCAAATGTGAGTCAACATTTTAAATTTATGTTCAAC 960
DB 919 TTTATATATTAACCTAGCTGCTATTCAAATGTGAGTCAACATTTTAAATTTATGTTCAAC 978
OY 961 TGTTTGTGAGACTGAAT 977
DB 979 TGTTTGTGAGACTGAAT 995

RESULT 11
ABX08764
ID ABX08764 standard; cDNA, 1142 BP.
AC ABX08764;
XX 21-JAN-2003 (first entry)
DE Angiogenesis-associated human polynucleotide sequence #26.
XX Human; angiogenesis-associated transcript; angiogenesis;
XX angiogenesis-associated disease; cancer; cytostatic; gene therapy; gene;
XX 88.
XX Homo sapiens.
XX OS
XX MO200279492-A2.
XX 10-OCT-2002.
XX 14-FEB-2002; 2002WO-US004915.
XX 14-FEB-2001; 2001US-00784356.
XX 22-FEB-2001; 2001US-00791399.
XX 19-APR-2001; 2001US-0285475P.
XX 03-AUG-2001; 2001US-0310025P.
XX 13-NOV-2001; 2001US-0350666P.
XX 29-NOV-2001; 2001US-0334244P.
XX
XX (E0SB-) EOS BIOTECHNOLOGY INC.
XX
XX Murray R, Glynn R, Watson SR, Aziz N,
XX
XX WPI; 2003-040681/03.
XX
XX P-PSDB; ABU03481.
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XX
PT Detecting angiogenesis-associated transcript in a cell for diagnosing and
PT treating cancer by contacting a sample with a polynucleotide that
PT exhibits changes in expression level as a function of time in tissue
PT undergoing angiogenesis.
XX
XX Example 2; Page 205; 291pp; English.
XX
XX The present invention relates to methods and compositions for detecting
XX an angiogenesis-associated transcript in a cell in a patient. The method
XX involves contacting a biological sample from the patient with a
XX polynucleotide that selectively hybridizes to a sequence at least 80%
XX identical to any of the angiogenesis-associated human polynucleotide
XX sequences given in the specification. These angiogenesis-associated
XX polynucleotide sequences comprise genes that exhibit changes in
XX expression levels as a function of time in tissue undergoing
XX angiogenesis. The method and the polynucleotide sequences of the
XX invention are useful for diagnosing and treating angiogenesis and
XX angiogenesis-associated diseases e.g. cancer. The polynucleotide
XX sequences are also useful in the gene therapy of such disorders. The
XX angiogenesis-associated proteins encoded by the polynucleotide sequences
XX are useful as a vaccine for therapeutic and prophylactic immunisation.
XX ABX08739-ABX08853 represent angiogenesis-associated polynucleotide
XX sequences
XX
SQ Sequence 1142 BP; 316 A; 248 C; 260 G; 318 T; 0 U; 0 Other;
XX
Query Match 99.3%; Score 972.2; DB 10; Length 1142;
Best Local Similarity 99.7%; Pred. No. 9.9e-255;
Matches 974; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 GGAAGCCTTGGCCAGCGGCGCGCCGACCCCTGACAGATGAGACCCGCTGCGCCCTGG 60
DB 19 GAGCGCTTGGCCAGCGGCGCGCCGACCCCTGACAGATGAGACCCGCTGCGCCCTGG 78
OY 61 GGCTGTGATTCGTGCTCTTTTCTGACGAGGCTGCACTGGGCGATGCTGCTCAGAGC 120
DB 79 GGCTGTGATTCGTGCTCTTTTCTGACGAGGCTGCACTGGGCGATGCTGCTCAGAGC 138
OY 121 CAACAGAAATTAACCGGAGATCTGTCTCTGCCCCCTGACTACGAGACCTTCCGGGCC 180
DB 139 CAACAGAAATTAACCGGAGATCTGTCTCTGCCCCCTGACTACGAGACCTTCCGGGCC 198
OY 181 TACTTCTCGTTACTACGACAGGTACAGGCTACGAGGCTGCGGAGTCCGTACGAGG 240
DB 199 TACTTCTCGTTACTACGACAGGTACAGGCTACGAGGCTGCGGAGTCCGTACGAGG 258
OY 241 GCTGGAAGGCAACGCAAAATTTCTACCTGTGGAGGCTTGCAGCATGCTTCTGGA 300
DB 259 GCTGGAAGGCAACGCAAAATTTCTACCTGTGGAGGCTTGCAGCATGCTTCTGGA 318
OY 301 GGATGAAAAAGTTCCAAAGTTTCCGGCTGCAAGTATGTGAGCAACAGTGTAGG 360
DB 319 GGATGAAAAAGTTCCAAAGTTTCCGGCTGCAAGTATGTGAGCAACAGTGTAGG 378
OY 361 GGTCAAGAAAAAGTATTTCTTAATCTAAGTTCATGACATGAGAAAAATCTTTTCCG 420
DB 379 GGTCAAGAAAAAGTATTTCTTAATCTAAGTTCATGACATGAGAAAAATCTTTTCCG 438
OY 421 GTGGGTTCACCGAACCAGATTGAGACAGGTTCCAGATGAACTATTGTATGGGCT 480
DB 439 GTGGGTTCACCGAACCAGATTGAGACAGGTTCCAGATGAACTATTGTATGGGCT 498
OY 481 TCTGGCCACCAAGAAATTCATCTTGTCTACAGTCCAAAAGATGAGGGACGTGTCT 540
DB 499 TCTGGCCACCAAGAAATTCATCTTGTCTACAGTCCAAAAGATGAGGGACGTGTCT 558
OY 541 CTGCCAATGTGACTGCTATTTATTTAATCCAAAGATGAGAACTGTGTCTTCACT 600
DB 559 CTGCCAATGTGACTGCTATTTATTTAATCCAAAGATGAGAACTGTGTCTTCACT 618
OY 601 ATACTGCTGTGAGGAGAAATGACATTAATCTTGTAGCAGGAGATTCGAAACGTGCAT 660
```

Db	61.9	ANATCGGCTGTGGAGGGAATGACAAATPACTTTGTAGACAGAGGAAATGCAACGTGCAT	678
Qy	661	GTGCAAAAGCTTTGAAAAAGAAAAAGATGCGCAAGCTTGGCTTGCGCAGTGAATCC	720
Db	679	GTGCAAAAGCTTTGAAAAAGAAAAAGATGCGCAAGCTTGGCTTGCGCAGTGAATCC	738
Qy	721	GGAAATTTGGGAAGAACATTTTAAACATCTTAAATATGTCATCTTGTGCTTTATG	780
Db	739	GGAAATTTGGGAAGAACATTTTAAACATCTTAAATATGTCATCTTGTGCTTTATG	788
Qy	781	GCTTATTTCCCTTATGTTGTATCTGAAGAAATATATGACACAGAGGAAACAAATCA	840
Db	799	GCTTATTTCCCTTATGTTGTATCTGAAGAAATATATGACACAGAGGAAACAAATCA	858
Qy	841	TTGGTGATTTATTCACCAAGTTTTTATTAATACAGTCACCTTTTCAAAAATTTGGATTT	900
Db	859	TTGGTGATTTATTCACCAAGTTTTTATTAATACAGTCACCTTTTCAAAAATTTGGATTT	918
Qy	901	TTTATATATACAGTCAGTCATTAATGAATGAGTCACTTTTAAATTAATGTTCAAC	960
Db	919	TTTATATATACAGTCAGTCATTAATGAATGAGTCACTTTTAAATTAATGTTCAAC	978
Qy	961	TGTTTGTGAGACTGAAT	977
Db	979	TGTTTGTGAGACTGAAT	995
RESULT 12			
ADN38705	ADN38705 standard; cDNA; 1142 BP.		
XX	ADN38705;		
DT	17-JUN-2004 (first entry)		
XX	Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:23.		
DE	Human; differential expression; cancer; angiogenic disorder;		
XX	Fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;		
KM	Inflammatory disease; autoimmune disease;		
KM	retinal neovascularisation syndrome; scarring; uterine fibroid;		
KW	detection; diagnosis; prognosis; drug screening; drug targeting;		
KM	wound healing; contraception; cytostatic; cardiac; immunomodulatory;		
XX	vulneraty; gene therapy; vaccine; gene; ss.		
OS	Homo sapiens.		
XX	WO2003042661-A2.		
PN	22-MAY-2003.		
XX	13-NOV-2002; 2002WO-US036810.		
PF	13-NOV-2001; 2001US-0350666P.		
XX	21-NOV-2001; 2001US-0332464P.		
PR	29-NOV-2001; 2001US-0334393P.		
PR	03-DEC-2001; 2001US-0335394P.		
PR	14-DEC-2001; 2001US-0340376P.		
PR	08-JAN-2002; 2002US-0347211P.		
PR	10-JAN-2002; 2002US-0347349P.		
PR	08-FEB-2002; 2002US-035520P.		
PR	13-FEB-2002; 2002US-0356714P.		
PR	20-FEB-2002; 2002US-0359077P.		
PR	29-MAR-2002; 2002US-036809P.		
PR	04-APR-2002; 2002US-0370110P.		
PR	12-APR-2002; 2002US-0372246P.		
PR	05-JUN-2002; 2002US-038614P.		
PR	16-JUL-2002; 2002US-0396839P.		
PR	22-JUL-2002; 2002US-039775P.		
PR	22-JUL-2002; 2002US-0397845P.		
PR	09-SEP-2002; 2002US-0409450P.		
XX	(BOSB-) EOS BIOTECHNOLOGY INC.		

XX	Afer D, Aziz N, Ginsburg WM, Glsh KC, Glyme R, Hevzi PA;
PI	Mack DJ, Murray R, Watson SR, Wilson KE, Ziolkni A;
XX	
DR	WPI; 2003-468649/44.
XX	P-PSTDB; ADN38706.
PT	Determining the presence or absence of a pathological cell in a patient,
XX	useful for diagnosing, prognosing or treating cancer, comprises detecting
XX	a nucleic acid in a biological sample.
PS	Claim 8; SEQ ID NO 23; 1385bp; English.
CC	The invention relates to nucleic acids and proteins (ADN38683-ADN40664)
CC	whose expression is upregulated or downregulated in specific cancers or
CC	other diseases such as angiogenic or fibrotic disorders, and to methods
CC	of determining the presence or absence of a pathological cell in a
CC	patient by detecting a nucleic acid at least 80% identical to those of
CC	the invention or by detecting a polypeptide of the invention. The
CC	invention also relates to expression vectors and host cells comprising a
CC	nucleic acid of the invention; antibodies which specifically bind a
CC	polypeptide of the invention; use of such antibodies for drug targeting;
CC	and methods of screening for modulators of activity or expression of the
CC	polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC	antibodies and methods are useful for diagnosing, prognosing and treating
CC	cancer and other conditions such as psoriasis, ischemia, heart disease,
CC	atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC	neovascularization syndromes, scarring and uterine fibroids. They may
CC	also be useful in wound healing and in contraception. The present
CC	sequence represents a nucleic acid sequence of the invention.
SEQ	Sequence 1142 BP; 316 A; 248 C; 260 G; 318 T; 0 U; 0 Other;
Query Match	99.3%; Score 972.2; DB 11; Length 1142;
Best Local Similarity	99.7%; P.No. 5.9e-256;
Matches 974; Conservative 3; Mismatch 35; Indels 0; Gaps 0;	
OY	1 GAAGCGCTTGGCCGACGGGCGGCCGACCCTTGACCATGAGACCCGCTGCCTGGCCTGG 60
DB	19 GAAGCGCTTGGCCGACGGGCGGCCGACCCTTGACCATGAGACCCGCTGCCTGGCCTGG 78
OY	61 GGCTGTGATTTCTGCTGTTTTCTGTACGAGAGGTGCACTGGGCGATGCTCTCAGAGC 120
DB	79 GGCTGTGATTTCTGCTGTTTTCTGTACGAGAGGTGCACTGGGCGATGCTCTCAGAGC 138
OY	121 CAACAGGAAAAAAGCGCGAGATCTGTCTCCCTTCAGATTAGAGAACCTTCGCGGCGCC 180
DB	139 CAACAGGAAAAAAGCGCGAGATCTGTCTCCCTTCAGATTAGAGAACCTTCGCGGCGCC 198
OY	181 TACTTCTCCGTTACTATACGACAGGTAACAAGAGAGTGCAGTCTCTGTACGAGG 240
DB	199 TACTTCTCCGTTACTATACGACAGGTAACAAGAGAGTGCAGTCTCTGTACGAGG 258
OY	241 GCTCGAGGGGCAACGCGCAAACTTTCTACACTTGGGAAGCTTTCGACGANTCTTGCTGA 300
DB	259 GCTCGAGGGGCAACGCGCAAACTTTCTACACTTGGGAAGCTTTCGACGANTCTTGCTGA 318
OY	301 GGATGAAAAAGTTCCCAAAGTTGGCGGCTGCAAGTAGAGTGTGACCAACAAGTGTAGG 360
DB	319 GGATGAAAAAGTTCCCAAAGTTGGCGGCTGCAAGTAGAGTGTGACCAACAAGTGTAGG 378
OY	361 GGTCACAGAAAAGTATTTCTTTATCTTAAGTTCATGACATGTGAAAAATTTCTTTCCG 420
DB	379 GGTCACAGAAAAGTATTTCTTTATCTTAAGTTCATGACATGTGAAAAATTTCTTTCCG 438
OY	421 GTGGGTGTACCGGAACCGGATTGAGAAGAGGTTTCAATGAAGACTATCTGTATGGCT 480
DB	439 GTGGGTGTACCGGAACCGGATTGAGAAGAGGTTTCAATGAAGACTATCTGTATGGCT 498
OY	481 TTCTGGCACCAAAAGAAATTCATCATTTTGTCTACAGTCCAAAGATGAGGAGCATGTGCT 540
DB	499 TTCTGGCACCAAAAGAAATTCATCATTTTGTCTACAGTCCAAAGATGAGGAGCATGTGCT 558

QY 541 CTGCCAATGTGACCTGCTATTATTTAAATCCAAAGATACAGACCTGTATGCTTCACCT 600  
DB 559 CTGCCAATGTGACCTGCTATTATTTAAATCCAAAGATACAGACCTGTATGCTTCACCT 618  
QY 601 ATACTGCTGTGAGAGGAATGCAATTAATCTTTAGCAGGAGGATTCGCAACCTGCAT 660  
DB 619 ATACTGCTGTGAGAGGAATGCAATTAATCTTTAGCAGGAGGATTCGCAACCTGCAT 678  
QY 661 GTGCAAAAGCTTTGAAAAAGAAAAAGAGATCCCAAGCTTGTGCTTGCAGTAGAATCC 720  
DB 679 GTGCAAAAGCTTTGAAAAAGAAAAAGAGATCCCAAGCTTGTGCTTGCAGTAGAATCC 738  
QY 721 GGAATAATTCGGAAGAAGCAATTTTAAACATCTTAATATGTCATCTGTGCTTTATG 780  
DB 739 GGAATAATTCGGAAGAAGCAATTTTAAACATCTTAATATGTCATCTGTGCTTTATG 798  
QY 781 GCTTATTTGCTTTATGCTTATGCTATGCAAGATTAATATGACAGATGAGAAACAATCA 840  
DB 799 GCTTATTTGCTTTATGCTTATGCTATGCAAGATTAATATGACAGATGAGAAACAATCA 858  
QY 841 TTGGTGATTTATTCACCAAGCTTTTATTAATACAGTCACTTTTCAAAAATTGCAATTT 900  
DB 859 TTGGTGATTTATTCACCAAGCTTTTATTAATACAGTCACTTTTCAAAAATTGCAATTT 918  
QY 901 TTTATATATTAATCTAGCTGCTATTCAAATGAGTCAACATTTTAAATTTATGTTCAAC 960  
DB 919 TTTATATATTAATCTAGCTGCTATTCAAATGAGTCAACATTTTAAATTTATGTTCAAC 978  
QY 961 TGTGTTGAGACTGAAT 977  
DB 979 TGTGTTGAGACTGAAT 995

RESULT 13  
ADL83254  
ID ADL83254 standard; cDNA; 1142 BP.  
XX  
AC ADL83254;  
XX  
DT 17-JUN-2004 (first entry)  
XX  
DE Human PRO35972 cDNA, SEQ ID 456.  
XX  
KM Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;  
KM Antiallergic; Muscular; Neuroprotective; Nephrotoxic; Antiinflammatory;  
KM Gene therapy; PRO; B cell related disorder; cancer;  
KM Immune-mediated inflammatory disease; human; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2004024097-A2.  
XX  
PD 25-MAR-2004.  
XX  
PF 15-SEP-2003; 2003WO-US029097.  
XX  
PR 16-SEP-2002; 2002US-0411392P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;  
PI Wu ID;  
XX  
DR WPI; 2004-329389/30.  
XX  
P P-PDB; ADL83255.  
XX  
PT New PRO polypeptide, useful for diagnosing and treating a B cell related  
PT disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune  
PT mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.  
XX  
PS Claim 2; Fig 456; 695BP; English.  
XX  
CC The present invention relates to PRO proteins and their coding sequences.

CC The PRO proteins are useful for diagnosing and treating a B cell related  
CC disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide  
CC antigen unresponsiveness, selective IgA deficiency, immunodeficiency with  
CC deficiency, selective deficiency of IgG subclasses, immunodeficiency with  
CC hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's  
CC lymphoma, intermediate lymphoma, follicular lymphoma, type II  
CC hypersensitivity, rheumatoid arthritis, autoimmune mediated hemolytic  
CC anemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or  
CC ankylosing spondylitis. The PRO proteins are also useful for preparing a  
CC medicament for treating a condition that is responsive to the PRO  
CC protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO  
CC coding sequences are useful as hybridization probes in chromosome and  
CC gene mapping, in preparing PRO proteins, or in generating transgenic  
CC animals or knockout animals, which in turn are useful in the development  
CC and screening of therapeutically useful reagents.  
XX  
SQ Sequence 1142 BP; 316 A; 248 C; 260 G; 318 T; 0 U; 0 Other;  
Query Match 99.3%; Score 972.2; DB 12; Length 1142;  
Best Local Similarity 99.7%; Pred. No. 9,9e-256;  
Matches 974; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GGACGCTTGGCCACGCGGCGCCGACCCCTGACCAATGACCCTGCGCCCTCG 60  
DB 19 GGAAGCTTGGCCACGCGGCGCCGACCCCTGACCAATGACCCTGCGCCCTCG 78  
QY 61 GGCTGTCAATTCGTGCTCTTTCTGACGAGGCTGCACTGGGCGAATGCTGTCAAGAC 120  
DB 79 GGCTGTCAATTCGTGCTCTTTCTGACGAGGCTGCACTGGGCGAATGCTGTCAAGAC 138  
QY 121 CAACGAGAAATPAGCGGAGATCTGCTCTGCCCCCTGACATGAGCAACCTGCGGGGCC 180  
DB 139 CAACGAGAAATPAGCGGAGATCTGCTCTGCCCCCTGACATGAGCAACCTGCGGGGCC 198  
QY 181 TACTTCTCGTTACTACTACAGATACAGCAGAGTCCGCGAGTTCCTGTAAGGGG 240  
DB 199 TACTTCTCGTTACTACTACAGATACAGCAGAGTCCGCGAGTTCCTGTAAGGGG 258  
QY 241 GCTGCGAGGCAAGCCCAACAAATTTCTACACTGGAGGCTTGCACATGCTTGTGTA 300  
DB 259 GCTGCGAGGCAAGCCCAACAAATTTCTACACTGGAGGCTTGCACATGCTTGTGTA 318  
QY 301 GGATAGAAAAAGTCCCAAGGTTGCGGAGTGCAGTGAAGTGTGACGACAGTGTGAGG 360  
DB 319 GGATAGAAAAAGTCCCAAGGTTGCGGAGTGCAGTGAAGTGTGACGACAGTGTGAGG 378  
QY 361 GGTCCACAGAAAGTATTTCTTAATCTAAGTTCATGACATGTGAAAAATTCCTTTCG 420  
DB 379 GGTCCACAGAAAGTATTTCTTAATCTAAGTTCATGACATGTGAAAAATTCCTTTCG 438  
QY 421 GTGGGTGACCGGAACCGGATGGAACAGGTTCCAGATGACACTTGTATGGGCT 480  
DB 439 GTGGGTGACCGGAACCGGATGGAACAGGTTCCAGATGACACTTGTATGGGCT 498  
QY 481 TCTGCGACCAAGAAATTCATATTTGTACAGTCCAAAGATGAGGAGCTGTGCT 540  
DB 499 TCTGCGACCAAGAAATTCATATTTGTACAGTCCAAAGATGAGGAGCTGTGCT 558  
QY 541 CTGCCAATGTGACCTGCTATTATTTAAATCCAAAGATACAGACCTGTATGCTTCACCT 600  
DB 559 CTGCCAATGTGACCTGCTATTATTTAAATCCAAAGATACAGACCTGTATGCTTCACCT 618  
QY 601 ATACTGCTGTGAGAGGAATGCAATTAATCTTTAGCAGGAGGATTCGCAACCTGCAT 660  
DB 619 ATACTGCTGTGAGAGGAATGCAATTAATCTTTAGCAGGAGGATTCGCAACCTGCAT 678  
QY 661 GTGCAAAAGCTTTGAAAAAGAAAAAGAGATCCCAAGCTTGTGCTTGCAGTAGAATCC 720  
DB 679 GTGCAAAAGCTTTGAAAAAGAAAAAGAGATCCCAAGCTTGTGCTTGCAGTAGAATCC 738  
QY 721 GGAATAATTCGGAAGAAGCAATTTTAAACATCTTAATATGTCATCTGTGCTTTATG 780  
DB 739 GGAATAATTCGGAAGAAGCAATTTTAAACATCTTAATATGTCATCTGTGCTTTATG 798

QY 761 GCTATTGCTTTAGTGTGATCTGAGAAATATGACAGCATGAGAAACAATCA 840  
DB 769 GCTATTGCTTTAGTGTGATCTGAGAAATATGACAGCATGAGAAACAATCA 858  
QY 841 TTGGGATTTATTCACCAATTTTATTAATACAGTCATTTTCAAAAATTGGATTTT 900  
DB 859 TTGGGATTTATTCACCAATTTTATTAATACAGTCATTTTCAAAAATTGGATTTT 918  
QY 901 TTTATATATACCTAGCTGCTATTCAAATGAGTCTACCATTTTATTTATGTTCAAC 960  
DB 919 TTTATATATACCTAGCTGCTATTCAAATGAGTCTACCATTTTATTTATGTTCAAC 978  
QY 961 TGTGTGAGACTGAT 977  
DB 979 TGTGTGAGACTGAT 995  
RESULT 14  
ID ADU06173 standard; DNA; 1142 BP.  
AC ADU06173;  
XX 27-JAN-2005 (first entry)  
DT Novel bronchial cancer-associated human gene SeqIDJ397.  
XX Novel bronchial cancer-associated human gene SeqIDJ397.  
XX bronchial cancer; cytostatic; tumour-associated protein;  
XX cancer detection; metastasis; tumour; gene; ds; human.  
XX Homo sapiens.  
XX DE10316701-A1.  
XX PD 04-NOV-2004.  
XX 09-APR-2003; 2003DE-01016701.  
XX PR 09-APR-2003; 2003DE-01016701.  
XX (HINZ/) HINZMANN B.  
PA (HERM/) HERMANN K.  
PA (CAST/) HEIDEN CASTANOS-VELEZ E.  
PI Mennerich D, Bruemendorf T, Heiden E, Hermann K, Kinnemann H;  
PI Li X, Roepcke S, Staub B, Hinzmann B, Rosenthal A, Pilarsky C;  
XX WPI; 2004-786403/78.  
DR P-PSDB; ADU06660.  
XX New nucleic acid, and derived proteins, useful for diagnosis of bronchial  
PT cancer and in screening for therapeutic and diagnostic agents.  
XX Claim 1; SEQ ID NO 397; 1381bp; German.  
CC This invention relates to a novel isolated nucleic acid associated with  
CC bronchial cancer comprising 489 defined sequences given in the  
CC specification. The invention may be useful for the production of  
CC compounds with a cytostatic activity through the inhibition of expression  
CC or activity of tumour-associated proteins. The novel DNA sequences and  
CC the proteins/peptides encoded by them are used for detecting bronchial  
CC cancer or determining the risk of developing it and to screen for  
CC specific binding partners of the DNA or protein sequences, where the  
CC binding partners are potentially useful as agents for treating or  
CC diagnosing bronchial cancer. The DNA or protein sequences can also be  
CC used for prognosis, detection of metastases and for secondary treatment  
CC (of tumours that have been stabilised or are no longer detectable).  
CC Detecting abnormal expression of the DNA sequences provides early  
CC diagnosis of bronchial cancers. The present sequence is that of a novel  
CC bronchial cancer-associated human gene sequence of the invention.  
XX Sequence 1142 BP; 316 A; 248 C; 260 G; 318 T; 0 U; 0 Other;

Query Match 99.3%; Score 972.2; DB 13; Length 1142;  
Best Local Similarity 99.7%; Pred. No. 9.9e-256;  
Matches 974; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GGAGCCCTTCCCGCAGCGGGCGCGCCGACCCCTGACCAATGACCCTGCGCCCTCG 60  
DB 19 GGACGCCCTTCCCGCAGCGGGCGCGCCGACCCCTGACCAATGACCCTGCGCCCTCG 78  
QY 61 GGCGTGCATTCGTGCTTTTCCGACGAGGGCTGCACTGGGGAGATGCTGTCAGAGGC 120  
DB 79 GGCGTGCATTCGTGCTTTTCCGACGAGGGCTGCACTGGGGAGATGCTGTCAGAGGC 138  
QY 121 CAACAGAAATPACGCGAGATCTGCTCTCGCCCTGAGCTACAGCACTTCCGCGGCC 180  
DB 139 CAACAGAAATPACGCGAGATCTGCTCTCGCCCTGAGCTACAGCACTTCCGCGGCC 198  
QY 181 TACTTCTCCGTTACTACTACAGATACAGCAAGTCCGCGCCGACGTTCTGTACGCG 240  
DB 199 TACTTCTCCGTTACTACTACAGATACAGCAAGTCCGCGCCGACGTTCTGTACGCG 258  
QY 241 GCTGAGGGGCAAGCGCAATTTCTACCTGGAGGCTTGGCAGATGCTTGGTGA 300  
DB 259 GCTGAGGGGCAAGCGCAATTTCTACCTGGAGGCTTGGCAGATGCTTGGTGA 318  
QY 301 GGATPAGAAAAGTTCCCAAGTTTCCGCGCTGCAAGTGAAGTGAAGCAAGTGTGAG 360  
DB 319 GGATPAGAAAAGTTCCCAAGTTTCCGCGCTGCAAGTGAAGTGAAGCAAGTGTGAG 378  
QY 361 GGTCCACGAAAAGTATTTCTTTATCTTAATCTCAATGCAATGTGAAAATTTCTTCCG 420  
DB 379 GGTCCACGAAAAGTATTTCTTTATCTTAATCTCAATGCAATGTGAAAATTTCTTCCG 438  
QY 421 GTGGGATGCAACCGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 480  
DB 439 GTGGGATGCAACCGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 498  
QY 481 TCTGCGCACCAAGAAAATTCATATTTTGTGCTACAGTCCAAAAGATGAGGAGCT 540  
DB 499 TCTGCGCACCAAGAAAATTCATATTTTGTGCTACAGTCCAAAAGATGAGGAGCT 558  
QY 541 CTGCAATGTGACCTGCTATTTTATTAATCCAAATACAACTGTGATGCTTCACT 600  
DB 559 CTGCAATGTGACCTGCTATTTTATTAATCCAAATACAACTGTGATGCTTCACT 618  
QY 601 ATACTGCTGTGAGGAGATGCAATATCTTTTGAAGGAGGATTTGCAAGTGCAT 660  
DB 619 ATACTGCTGTGAGGAGATGCAATATCTTTTGAAGGAGGATTTGCAAGTGCAT 678  
QY 661 GTGCAAAAGCTTTGAAAAGAAAAGAAAGATCCAAAGCTTGTGCTGCAATGATCC 720  
DB 679 GTGCAAAAGCTTTGAAAAGAAAAGAAAGATCCAAAGCTTGTGCTGCAATGATCC 738  
QY 721 GGAAAATTCGAGAAAGCAATTTTAACTTTTAATATGATCTGTTGCTTTATG 780  
DB 739 GGAAAATTCGAGAAAGCAATTTTAACTTTTAATATGATCTGTTGCTTTATG 798  
QY 781 GCTATTGCTTTATGTTGATCTGAAAGAAATATGACAGATGAGAAACAATCA 840  
DB 799 GCTATTGCTTTATGTTGATCTGAAAGAAATATGACAGATGAGAAACAATCA 858  
QY 841 TTGGTGAATTTATTCACCAATTTTATTAATACAGTCATTTTCAAAAATTGGATTTT 900  
DB 859 TTGGTGAATTTATTCACCAATTTTATTAATACAGTCATTTTCAAAAATTGGATTTT 918  
QY 901 TTTATATATACCTAGCTGCTATTCAAATGAGTCTACCATTTTATTTATGTTCAAC 960  
DB 919 TTTATATATACCTAGCTGCTATTCAAATGAGTCTACCATTTTATTTATGTTCAAC 978  
QY 961 TGTGTGAGACTGAT 977  
DB 979 TGTGTGAGACTGAT 995



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OM nucleic - nucleic search, using sw model

Run on: March 11, 2006, 05:30:18 ; Search time 4764 Seconds  
(without alignments)  
9614.726 Million cell updates/sec

Title: US-10-800-057-1

Perfect score: 979  
Sequence: 1 ggaacgcttcgacgagcgggc.....ctgttgcgagacgacatc 979

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
EST:\*  
1: gb\_esc1:\*  
2: gb\_esc2:\*  
3: gb\_esc3:\*  
4: gb\_esc4:\*  
5: gb\_esc5:\*  
6: gb\_esc6:\*  
7: gb\_esc7:\*  
8: gb\_esc8:\*  
9: gb\_esc9:\*  
10: gb\_esc10:\*  
11: gb\_esc11:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	978.6	100.0	1104	1	AL551975
2	977.4	99.8	1002	4	CR601552
3	977.4	99.8	1006	4	CR605727
4	977.4	99.8	1007	4	CR615838
5	977.4	99.8	1009	4	CR620705
6	977.4	99.8	1028	4	CR621703
7	977.4	99.8	1031	4	CR615468
8	977.4	99.8	1033	4	CR612082
9	977.4	99.8	1034	4	CR601201
10	977.4	99.8	1038	4	CR618958
11	977.4	99.8	1039	4	CR624861
12	977.4	99.8	1042	4	CR621074
13	977.4	99.8	1046	4	CR611856
14	977.4	99.8	1047	4	CR605333
15	977.4	99.8	1050	4	CR607266
16	977.4	99.8	1053	4	CR618532
17	977.4	99.8	1058	4	CR594877
18	977.4	99.8	1111	4	CR617744
19	977.4	99.8	1115	4	CR608970
20	977.4	99.8	1119	4	CR592954
21	977.4	99.8	1120	4	CR594855
22	977.4	99.8	1120	4	CR597838

23	977.4	99.8	1124	4	CR591910	CR591910 full-length
24	977.4	99.8	1126	4	CR609583	CR609583 full-length
25	977.4	99.8	1127	4	CR612450	CR612450 full-length
26	977.4	99.8	1134	4	CR593701	CR593701 full-length
27	977.4	99.8	1134	4	CR599406	CR599406 full-length
28	977.4	99.8	1139	4	CR593463	CR593463 full-length
29	977.4	99.8	1139	4	CR626794	CR626794 full-length
30	977.4	99.8	1140	4	CR620763	CR620763 full-length
31	977.4	99.8	1144	4	CR611193	CR611193 full-length
32	977.4	99.8	1145	4	CR596932	CR596932 full-length
33	977.4	99.8	1146	4	CR608257	CR608257 full-length
34	977.4	99.8	1146	4	CR613976	CR613976 full-length
35	977.4	99.8	1147	4	CR606533	CR606533 full-length
36	977.4	99.8	1150	4	CR607204	CR607204 full-length
37	977.4	99.8	1150	4	CR619096	CR619096 full-length
38	977.4	99.8	1151	4	CR593891	CR593891 full-length
39	977.4	99.8	1151	4	CR603850	CR603850 full-length
40	977.4	99.8	1156	4	CR597697	CR597697 full-length
41	977.4	99.8	1161	4	CR591590	CR591590 full-length
42	977.4	99.8	1165	4	CR594214	CR594214 full-length
43	977.4	99.8	1196	4	CR597321	CR597321 full-length
44	977.4	99.8	1339	4	CR592379	CR592379 full-length
45	977.4	99.8	1366	4	CR595356	CR595356 full-length

#### ALIGNMENTS

RESULT 1  
AL551975 1104 bp mRNA linear EST 30-MAR-2004  
LOCUS AL551975 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
DEFINITION clone CSOD1060YJ11 5-PRIME, mRNA sequence.  
ACCESSION AL551975 GI:45856764  
VERSION AL551975.3  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 1104)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
On Feb 15, 2001 this sequence version replaced gi:31273791.

REFERENCE  
AUTHORS  
TITLES  
JOURNAL  
COMMENT  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
4300.r

For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?c=CSOD1060YJ11&c=4300.r.

#### FEATURES

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/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="CSOD1060YJ11"  
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/clone\_11b="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

#### ORIGIN

Query Match 100.0%; Score 979; DB 1; Length 1104;

Best Local Similarity 99.9%; Pred. No. 7.8e-244; Matches 978; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGAGCGCTTGCCGACGCGGCGCCGACCCCTGACACATGACACCCGCTGCGCCCTG 60
Db 21 GGAGCGCTTGCCGACGCGGCGCCGACCCCTGACACATGACACCCGCTGCGCCCTG 80
QY 61 GGCTGTGATTTCTGCTGCTTTTCTGACGAGGCTGCACTGGGCGATGCTGCTCAGAGC 120
Db 81 GGCTGTGATTTCTGCTGCTTTTCTGACGAGGCTGCACTGGGCGATGCTGCTCAGAGC 140
QY 121 CAACGAGAAATACGCGGAGATCTGCTCTGCGCCCTAGACTACGAGACCTGCGCGGCC 180
Db 141 CAACGAGAAATACGCGGAGATCTGCTCTGCGCCCTAGACTACGAGACCTGCGCGGCC 200
QY 181 TACTTCTCCGTTACTACTACGACAGGTACACGACAGCTGCGCGCAGTTCTGTACGGG 240
Db 201 TACTTCTCCGTTACTACTACGACAGGTACACGACAGCTGCGCGCAGTTCTGTACGGG 260
QY 241 GCTGCGAGGGCAACGCGCAACATTTCTACACCTGGAGGCTTGCGACGATGCTGTGGA 300
Db 261 GCTGCGAGGGCAACGCGCAACATTTCTACACCTGGAGGCTTGCGACGATGCTGTGGA 320
QY 301 GGATGAGAAAGTTTCCCAAGTTTGGCGGCTGCAATGAGTGTGACACGATGTGAG 360
Db 321 GGATGAGAAAGTTTCCCAAGTTTGGCGGCTGCAATGAGTGTGACACGATGTGAG 380
QY 361 GGTCCACAGAAAAGTATTTCTTAACTTAAGTTCATGACATGTGAAAATTTCTTTCCG 420
Db 381 GGTCCACAGAAAAGTATTTCTTAACTTAAGTTCATGACATGTGAAAATTTCTTTCCG 440
QY 421 GTGGGTGTCAACCGGAACCGGATTTAGAACAGGTTTCCAGATGAAAGTACTGTATG 480
Db 441 GTGGGTGTCAACCGGAACCGGATTTAGAACAGGTTTCCAGATGAAAGTACTGTATG 500
QY 481 TGTGGGCAACAAAGAAATTTTCATCATTTTGTGCTACAGTCCAAAAGATGAGGACTGT 540
Db 501 TGTGGGCAACAAAGAAATTTTCATCATTTTGTGCTACAGTCCAAAAGATGAGGACTGT 560
QY 541 CTGCCAATGTGACTGCTATTTATTTTAACTCAAGATACAGAACTGTGATGCTTACCT 600
Db 561 CTGCCAATGTGACTGCTATTTATTTTAACTCAAGATACAGAACTGTGATGCTTACCT 620
QY 601 AATCTGCTGTGAGGAAATGACAAATACCTTTGTGACGAGGAGATTCGAAACGTCAT 660
Db 621 AATCTGCTGTGAGGAAATGACAAATACCTTTGTGACGAGGAGATTCGAAACGTCAT 680
QY 661 GTGCAAAAGCTTTGAAAAGAAAAGAAATGCGAAAGCTTGGCTTGGCAATGAAATCC 720
Db 681 GTGCAAAAGCTTTGAAAAGAAAAGAAATGCGAAAGCTTGGCTTGGCAATGAAATCC 740
QY 721 GGAATAATTCGAGAAAGCAATTTTAAACATTTCTTAATATGTCACTGTGTTGCTTATG 780
Db 741 GGAATAATTCGAGAAAGCAATTTTAAACATTTCTTAATATGTCACTGTGTTGCTTATG 800
QY 781 GCTTATTTGCTTTATGTTGTATCTGAAGAAATATATGACAGATGAGAGAAACAATCA 840
Db 801 GCTTATTTGCTTTATGTTGTATCTGAAGAAATATATGACAGATGAGAGAAACAATCA 860
QY 841 TTGGTGATTTATTCACAGTTTATTTATATACAGTCACTTTTCAAAAATTTGATTTT 900
Db 861 TTGGTGATTTATTCACAGTTTATTTATATACAGTCACTTTTCAAAAATTTGATTTT 920
QY 901 TTTATATATATACAGTCTATTTCAAAATGATGATCAACATTTTAAATTTATGTTTCAAC 960
Db 921 TTTATATATATACAGTCTATTTCAAAATGATGATCAACATTTTAAATTTATGTTTCAAC 980
QY 961 TGTGTGTGAGACTGAATTC 979
Db 981 TGTGTGTGAGACTGAATTC 999
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RESULT 2

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CR601552
LOCUS CR601552 1002 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CSOD1036YK11 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR601552
VERSION CR601552.1 GI:50482359
KEYWORDS HTC; CNSLT; cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 1002)
Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@liffech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Paradise Avenue
2 (bases 1 to 1002)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source Location/Qualifiers
1..1002
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="CSOD1036YK11"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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Query Match 99.8%; Score 977.4; DB 4; Length 1002;
Best Local Similarity 99.9%; Pred. No. 1.6e-243;
Matches 978; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGAGCGCTTGCCGACGCGGCGCCGACCCCTGACACATGACACCCGCTGCGCCCTG 60
Db 3 GGAGCGCTTGCCGACGCGGCGCCGACCCCTGACACATGACACCCGCTGCGCCCTG 62
QY 61 GGCTGTGATTTCTGCTGCTTTTCTGACGAGGCTGCACTGGGCGATGCTGCTCAGAGC 120
Db 63 GGCTGTGATTTCTGCTGCTTTTCTGACGAGGCTGCACTGGGCGATGCTGCTCAGAGC 122
QY 121 CAACGAGAAATACGCGGAGATCTGCTCTGCGCCCTAGACTACGAGACCTGCGCGGCC 180
Db 123 CAACGAGAAATACGCGGAGATCTGCTCTGCGCCCTAGACTACGAGACCTGCGCGGCC 182
QY 181 TACTTCTCCGTTACTACTACGACAGGTACACGACAGCTGCGCGCAGTTCTGTACGGG 240
Db 183 TACTTCTCCGTTACTACTACGACAGGTACACGACAGCTGCGCGCAGTTCTGTACGGG 242
QY 241 GCTGCGAGGGCAACGCGCAACATTTCTACACCTGGAGGCTTGCGACGATGCTGTGGA 300
Db 243 GCTGCGAGGGCAACGCGCAACATTTCTACACCTGGAGGCTTGCGACGATGCTGTGGA 302
QY 301 GGATGAGAAAGTTTCCCAAGTTTGGCGGCTGCAATGAGTGTGACACGATGTGAG 360
Db 303 GGATGAGAAAGTTTCCCAAGTTTGGCGGCTGCAATGAGTGTGACACGATGTGAG 362
QY 361 GGTCCACAGAAAAGTATTTCTTAACTTAAGTTCATGACATGTGAAAATTTCTTTCCG 420
Db 363 GGTCCACAGAAAAGTATTTCTTAACTTAAGTTCATGACATGTGAAAATTTCTTTCCG 422
QY 421 GTGGGTGTCAACCGGAACCGGATTTAGAACAGGTTTCCAGATGAAAGTACTGTATG 480
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Db 423 GTGGGATGACCGGAAACCGGATTTGAGAACAGGTTTCAGATGAGTACTGTATGAGGCT 482
Qy 481 TCTGGGACCAAAAGAAATTCATCATTTTGTCTACAGTCACAAAGATGAGGAGCTGTGCT 540
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Qy 541 CTGCCAATGTGACTGCTATTTATTTAAATCCAAAGATGAGGAGCTGTGATGCTTCACT 600
Db 543 CTGCCAATGTGACTGCTATTTATTTAAATCCAAAGATGAGGAGCTGTGATGCTTCACT 602
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Db 603 ATACTGCTGTGAGGAGGATGACAAATTAATCTTTGAGAGGAGATTCGCAACGTGCAAT 662
Qy 661 GTGCAAAAGCTTTGAAAAAGAAAAAGAGATGCAAGCTTGTGCTTGTGCAATGATCC 720
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Db 723 GGAATAATCGGAAGAGCAATTTTAAACATCTTAAATATGATCATCTGTGTTGCTTATG 782
Qy 781 GCTTATTTGCTTTATGTTGTTGATCTGAGAAATTAATATGACAGATGAGAAACAAATCA 840
Db 783 GCTTATTTGCTTTATGTTGTTGATCTGAGAAATTAATATGACAGATGAGAAACAAATCA 842
Qy 841 TTGGTATTTATTCACACGATTTTATTAATACAGTCACTTTTTCAAAAATTTGATTTT 900
Db 843 TTGGTATTTATTCACACGATTTTATTAATACAGTCACTTTTTCAAAAATTTGATTTT 902
Qy 901 TTTATATATTAATAGTGTGATTTCAAAATGAGTCAACATTTTAAATTTAATGTTCAAC 960
Db 903 TTTATATATTAATAGTGTGATTTCAAAATGAGTCAACATTTTAAATTTAATGTTCAAC 962
Qy 961 TGTGTTGAGACTGAAATTC 979
Db 963 TGTGTTGAGACTGAAATTC 981

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RESULT 3
CR605727 1006 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0D1042Yp21 of Placenta Cot 25-normalized
DEFINITION
ACCESSION CR605727
VERSION CR605727.1 GI:50486534
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 1006)
L1.W.B., Gruber,C., Jessee,J. and Polyes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 1006)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of invitrogen.
FEATURES
Location/Qualifiers
source 1..1006

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Query Match 99.8%; Score 977.4; DB 4; Length 1006;
Best Local Similarity 99.8%; Pred.No.1.6e-243;
Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GGAAGCCCTTGGCCAGCGGGCCGCCGACCCCTGACACATGAGACCCCGCTGCCCCCTGG 60
Db 26 GGAAGCCCTTGGCCAGCGGGCCGCCGACCCCTGACACATGAGACCCCGCTGCCCCCTGG 85
Qy 61 GGGTGTGATTTCTGCTCTTTTCTGACGAGAGGCTGACCTGGGCGATGCTGCTCAGAGAC 120
Db 86 GGGTGTGATTTCTGCTCTTTTCTGACGAGAGGCTGACCTGGGCGATGCTGCTCAGAGAC 145
Qy 121 CAACAGAAATTAACCGGAGATCTGTCTCCGCTGACCTAAGACCTAAGACCCGCGGCC 180
Db 146 CAACAGAAATTAACCGGAGATCTGTCTCCGCTGACCTAAGACCTAAGACCCGCGGCC 205
Qy 181 TACTTCTCCGTTACTACTACAGAGTACAGAGTACAGAGTACAGAGTACAGAGTACAGAG 240
Db 206 TACTTCTCCGTTACTACTACAGAGTACAGAGTACAGAGTACAGAGTACAGAGTACAGAG 265
Qy 241 GCTGCGAGGCGAAGCGCAAAATTTCTACACTGTGAGGCTTGTGCAAGATGCTTGTGCA 300
Db 266 GCTGCGAGGCGAAGCGCAAAATTTCTACACTGTGAGGCTTGTGCAAGATGCTTGTGCA 325
Qy 301 GGAATGAAAAATTTCCCAAGTTTCCCGCTGCAAGTGTGAGAGCAAGCAAGTGTGAGAG 360
Db 326 GGAATGAAAAATTTCCCAAGTTTCCCGCTGCAAGTGTGAGAGCAAGCAAGTGTGAGAG 385
Qy 361 GGTCCACAGAAAGATTTCTTAAATCTAAGTTCATGATGATGATGATGATGATGATGATG 420
Db 386 GGTCCACAGAAAGATTTCTTAAATCTAAGTTCATGATGATGATGATGATGATGATGATG 445
Qy 421 GTGGGATGACCGGAAACCGGATTTGAGAACAGGTTTCCAGATGAGTACTTGTATGAGGCT 480
Db 446 GTGGGATGACCGGAAACCGGATTTGAGAACAGGTTTCCAGATGAGTACTTGTATGAGGCT 505
Qy 481 TCTGGGACCAAAAGAAATTCATCATTTTGTCTACAGTCACAAAGATGAGGAGCTGTGCT 540
Db 506 TCTGGGACCAAAAGAAATTCATCATTTTGTCTACAGTCACAAAGATGAGGAGCTGTGCT 565
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Qy 601 ATACTGCTGTGAGGAGGATGACAAATTAATCTTTGAGAGGAGATTCGCAACGTGCAAT 660
Db 626 ATACTGCTGTGAGGAGGATGACAAATTAATCTTTGAGAGGAGATTCGCAACGTGCAAT 685
Qy 661 GTGCAAAAGCTTTGAAAAAGAAAAAGAGATGCAAGCTTGTGCTTGTGCAAGTATCC 720
Db 686 GTGCAAAAGCTTTGAAAAAGAAAAAGAGATGCAAGCTTGTGCTTGTGCAAGTATCC 745
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Qy 781 GCTTATTTGCTTTATGTTGTTGATCTGAGAAATTAATATGACAGATGAGAAACAAATCA 840
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Qy 841 TTGGTATTTATTAATAGTGTGATTTCAAAATGAGTCAACATTTTCAAAATTTGATTTT 900
Db 866 TTGGTATTTATTAATAGTGTGATTTCAAAATGAGTCAACATTTTCAAAATTTGATTTT 925
Qy 901 TTTATATATTAATAGTGTGATTTCAAAATGAGTCAACATTTTCAAAATTTAATGTTCAAC 960

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Db	926	TTTAAATATTAAGTACTGCTATTCAAATGTAAGTCTACCATTTTAAATTAATGTTCAAC	985
Oy	961	TGTTTGTGAGACTGAATTC	979
Db	986	TGTTTGTGAGACTGAATTC	1004
RESULT 4			
LOCUS	CR615838		
DEFINITION	full-length cDNA clone CSUDI075YF03 of Placenta Cot 25-normalized		
ACCESSION	CR615838		
VERSION	CR615838.1		
KEYWORDS	HTC; CNSLT cDNA.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Li, W.B., Gruber, C., Jesssee, J. and Poljays, D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	unpublished		
REMARK	Contact : Feng Liang Email : fliang@infotech.com URL : <a href="http://fulllength.invitrogen.com/">http://fulllength.invitrogen.com/</a> Invitrogen Corporation 1600 Paraday Avenue		
REFERENCE	2 (bases 1 to 1007)		
AUTHORS	Genoscope.		
TITLE	Direct Submiesage		
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : <a href="mailto:segre@genoscope.cns.fr">segre@genoscope.cns.fr</a> )		
COMMENT	1 - Web : <a href="http://www.genoscope.cns.fr">www.genoscope.cns.fr</a>		
FEATURES	1st strand cDNA was primed with a NotI-oligo(dt) primer. Five primes end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.		
SOURCE	Location/Qualifiers		
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	/clone_type="Placenta Cot 25-normalized"		
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Query Match	99.8%	Score 977.4	DB 4	Length 1007
Best Local Similarity	99.9%	Pred. No. 1,66-243		
Matches 978	Conservative 0	Mismatches 1	Indels 0	Gaps 0
QY	1	GAAGCCTCTGGCCAGCGGGCCGCGCCGACCCCTGTGACCATGAGCCCGCTGCGCCCTCTGG	60	
Db	3	GGAAGCCTCTGGCCAGCGGGCCGCGCCGACCCCTGTGACCATGAGCCCGCTGCGCCCTCTGG	62	
QY	61	GGCTGTGCAATCTGTGCTTTTCTCTGAGAGGAGCTGCACTGGGGCAATGTGCTCAGAGAC	120	
Db	63	GGCTGTCAATCTGTGCTTTTCTCTGAGAGGAGCTGCACTGGGGCAATGTGCTCAGAGAC	122	
QY	121	CAACAGGAATATACGCGAGATCTGTCTGCGCCCTGATACATACGAGACCTCTCGCGAGCC	180	
Db	123	CAACAGGAATATACGCGAGATCTGTCTGCGCCCTGATACATACGAGACCTCTCGCGAGCC	182	
QY	181	TACTTCTCCGTTACTACTACAGAGATACAGCAGAGCTGCCCGCAGTTCTCTGACGAGG	240	
Db	183	TACTTCTCCGTTACTACTACAGAGATACAGCAGAGCTGCCCGCAGTTCTCTGACGAGG	242	
QY	241	GCTCGAGAGGCAAGCGCAACAATTCTACACTGTGGAGAGCTTGGACATGCTGTCTGCA	300	
Db	243	GCTCGAGAGGCAAGCGCAACAATTCTACACTGTGGAGAGCTTGGACATGCTGTCTGCA	302	

QY	301	GGATGAGAAAAAGTTCCCAAGTTGGCCGGCTGCAGATGATGTGGACCAACAGTGTGAG	360
Db	303	GGATGAGAAAAAGTTCCCAAGTTGGCCGGCTGCAGATGATGTGGACCAACAGTGTGAG	362
QY	361	GGTCCACAGAAAAAGTATTTCTTAAATCTAAGTTCATGACATGTGAAAAATTCCTTTCCG	420
Db	363	GOTCCACAGAAAAAGTATTTCTTAAATCTAAGTTCATGACATGTGAAAAATTCCTTTCCG	422
QY	421	GTGGGTGTCAACCGGAAACCGGATTTGAGAACAGTTTCCAGATGAACTACTTGTATGGGCT	480
Db	423	GTGGGTGTCAACCGGAAACCGGATTTGAGAACAGTTTCCAGATGAACTACTTGTATGGGCT	482
QY	481	TCGTGCAACCAAGAAAAATTCATCATTTTGCTACAGTCCAAAAGATAGGAGCATGTGCT	540
Db	483	TCGTGCAACCAAGAAAAATTCATCATTTTGCTACAGTCCAAAAGATAGGAGCATGTGCT	542
QY	541	CTGCCAATGTGACTGTGCTATTTATTTAAATCCAGATACAGAACTGTGATGCTTTCACCT	600
Db	543	CTGCCAATGTGACTGTGCTATTTATTTAAATCCAGATACAGAACTGTGATGCTTTCACCT	602
QY	601	ATATCGGCTGTGAGGGAGATGACAATACTTGTTAGAGGAGGATTTGCAAACGTGCAT	660
Db	603	ATATCGGCTGTGAGGGAGATGACAATACTTGTTAGAGGAGGATTTGCAAACGTGCAT	662
QY	661	GTGCAAAAGCTTTGAAAAAGAAAAAGAAAGATGCCAAAGCTTGTGCTTTCACAGTAATCC	720
Db	663	GTGCAAAAGCTTTGAAAAAGAAAAAGAAAGATGCCAAAGCTTGTGCTTTCACAGTAATCC	722
QY	721	GGAAAAATTCGGAGAAAGCAATTTTAAACATCTTAAATATGATCATCTGTGTTGCTTTATG	780
Db	723	GGAAAAATTCGGAGAAAGCAATTTTAAACATCTTAAATATGATCATCTGTGTTGCTTTATG	782
QY	781	GCTTATTTGCTTTATGTTGTGTATCTGAAAGATATATAGACAGCATGAGAAACAATCA	840
Db	783	GCTTATTTGCTTTATGTTGTGTATCTGAAAGATATATAGACAGCATGAGAAACAATCA	842
QY	841	TTTGATGATTAATTCACACGTTTTTATTAATCAAGTCACTTTTCAAAAAATTTGATTTT	900
Db	843	TTTGATGATTAATTCACACGTTTTTATTAATCAAGTCACTTTTCAAAAAATTTGATTTT	902
QY	901	TTTATATATATACAGTGTCTAATTCAAATGTGAGTCAACATTTTAAATTAATTTATGTTCAAC	960
Db	903	TTTATATATATACAGTGTCTAATTCAAATGTGAGTCAACATTTTAAATTAATTTATGTTCAAC	962
QY	961	TGTTTGTGAGCTGAATTC 979	
Db	963	TGTTTGTGAGCTGAATTC 981	

[illegible]

## COMMENT

BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen.

## FEATURES

Location/Qualifiers  
 1..1009

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS0D1064YL18"  
 /issue\_type="Placenta Cot 25-normalized"  
 /plasmid="pCMVSPORT\_6"

## ORIGIN

Query Match 99.8%; Score 977.4; DB 4; Length 1009;  
 Best Local Similarity 99.9%; Pred. No. 1.6e-243;  
 Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 GGAGCGCTTTGCCAGCGGGCGCGCCGACCCCTGACACATGACCCCGCTGCGCCCTGG 60  
 20 GGACCGCTTGGCCAGCGGGCGCGCCGACCCCTGACACATGACCCCGCTGCGCCCTGG 79  
 61 GGCTGCTGATTTGCTGCTTTTCTGACGAGGCTGCACTGGGCGCATGCTGCTCAGAGAC 120  
 80 GGCTGCTGATTTGCTGCTTTTCTGACGAGGCTGCACTGGGCGCATGCTGCTCAGAGAC 139  
 121 CAACGAGAAATACCGGAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
 140 CAACGAGAAATACCGGAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 199  
 181 TACTTCTCCGTTACTACTACGACAGGTACACGAGAGCTGCGCCGATTCCTGTAAGGAG 240  
 200 TACTTCTCCGTTACTACTACGACAGGTACACGAGAGCTGCGCCGATTCCTGTAAGGAG 259  
 241 GCTGCGAGGCGCAACCGCAATTTTACACCTGCGAGGCTTCCAGCATGCTGCTGCTG 300  
 260 GCTGCGAGGCGCAACCGCAATTTTACACCTGCGAGGCTTCCAGCATGCTGCTGCTG 319  
 301 GGATGAGAAAGATTCCTCAAGTTTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
 320 GGATGAGAAAGATTCCTCAAGTTTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 379  
 361 GGATGAGAAAGATTCCTCAAGTTTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
 380 GGATGAGAAAGATTCCTCAAGTTTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 439  
 421 GTCGGGTGTCACCGGAAACCGGATTTGAGACAGGTTTCCAGTGAAGCTTATGATGGGCT 480  
 440 GTCGGGTGTCACCGGAAACCGGATTTGAGACAGGTTTCCAGTGAAGCTTATGATGGGCT 499  
 481 TCGGCGCACCAAGAAATTCATCTTTTGTCTACAGTCCAAAGATGAGGAGCTGTGCT 540  
 500 TCGGCGCACCAAGAAATTCATCTTTTGTCTACAGTCCAAAGATGAGGAGCTGTGCT 559  
 541 CTGCGCATGTGACTCGCTATTTTATTCAGATACAGAACTGTGATGCTTTGACCT 600  
 560 CTGCGCATGTGACTCGCTATTTTATTCAGATACAGAACTGTGATGCTTTGACCT 619  
 601 ATACTGGCTGTGAGGGAATGACATTAATCTTTTGTGACGAGGAGATTTGCAACGTGCA 660  
 620 ATACTGGCTGTGAGGGAATGACATTAATCTTTTGTGACGAGGAGATTTGCAACGTGCA 679  
 661 GTGCAAAAGCTTTGAAAAGAAAAGAAAGTCCAAAGCTTGTGCTGCAAGATGCT 720  
 680 GTGCAAAAGCTTTGAAAAGAAAAGAAAGTCCAAAGCTTGTGCTGCAAGATGCT 739  
 721 GGAATAATCGAAGAAAGCAATTTTAAACATCTTAAATATGTCATCTTGTGCTTTATG 780  
 740 GGAATAATCGAAGAAAGCAATTTTAAACATCTTAAATATGTCATCTTGTGCTTTATG 799

QY 781 GCTATTTGCTTTATGTTGATCTGAGATTAATATGACAGATGAGAAACAAATCA 840  
 DB 800 GCTATTTGCTTTATGTTGATCTGAGATTAATATGACAGATGAGAAACAAATCA 859

QY 841 TTGATGATTTATTCACGAGTTTATTAATACAGTCACTTTTCAAAAATTTGATTT 900  
 DB 860 TTGATGATTTATTCACGAGTTTATTAATACAGTCACTTTTCAAAAATTTGATTT 919

QY 901 TTTATATATATCTAGCTGATTTCAAAATGAGTCTACATTTTATTAATGATTTCAAC 960  
 DB 920 TTTATATATATCTAGCTGATTTCAAAATGAGTCTACATTTTATTAATGATTTCAAC 979

QY 961 TGTGTTGAGACTGAATTC 979  
 DB 980 TGTGTTGAGACTGAATTC 998

RESULT 6  
 CR621703 1028 bp mRNA linear HTC 21-JUL-2004  
 LOCUS full-length cDNA clone CS0D1031YL22 of Placenta Cot 25-normalized  
 DEFINITION of Homo sapiens (human).

ACCESSION CR621703  
 VERSION CR621703.1 GI:50502510  
 KEYWORDS HTC; CNSLT cDNA.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.

REFERENCE 1 (bases 1 to 1028)  
 AUTHORS Li,W.B., Gruber,C., Jessee,J. and Poyles,D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished  
 CONTACT : Feng Liang Email : fliang@lifetech.com URL :  
 REMARK http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
 Faraday Avenue

2 (bases 1 to 1028)

REFERENCE  
 AUTHORS Direct Submision  
 TITLE Genoscope.  
 JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

COMMENT BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen.

Location/Qualifiers

1..1028  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS0D1031YL22"  
 /issue\_type="Placenta Cot 25-normalized"  
 /plasmid="pCMVSPORT\_6"

## ORIGIN

Query Match 99.8%; Score 977.4; DB 4; Length 1028;  
 Best Local Similarity 99.9%; Pred. No. 1.6e-243;  
 Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 GGAGCGCTTTGCCAGCGGGCGCGCCGACCCCTGACACATGACCCCGCTGCGCCCTGG 60  
 20 GGACCGCTTGGCCAGCGGGCGCGCCGACCCCTGACACATGACCCCGCTGCGCCCTGG 88  
 61 GGCTGCTGATTTGCTGCTTTTCTGACGAGGCTGCACTGGGCGCATGCTGCTCAGAGAC 120  
 80 GGCTGCTGATTTGCTGCTTTTCTGACGAGGCTGCACTGGGCGCATGCTGCTCAGAGAC 148  
 121 CAACGAGAAATACCGGAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
 149 CAACGAGAAATACCGGAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 208

QY 181 TACTTCTCCGTTACTACGACAGGTACACGACAGCTGCGCCAGTTCCTGTACGGGG 240  
DB 209 TACTTCTCCGTTACTACGACAGGTACACGACAGCTGCGCCAGTTCCTGTACGGGG 268  
QY 241 GGTGCGAGGCGACACGACAAATTTCTACACCTGGAGGTTTCCGACGATGCTGTGCA 300  
DB 269 GGTGCGAGGCGACACGACAAATTTCTACACCTGGAGGTTTCCGACGATGCTGTGCA 328  
QY 301 GGATGAGAAAAAGTTCCCAAGTTTGGCGGTGCAAGTGTGACGACAGTGTGAG 360  
DB 329 GGATGAGAAAAAGTTCCCAAGTTTGGCGGTGCAAGTGTGACGACAGTGTGAG 388  
QY 361 GGTGCGACAGAAAGTATTTCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTT 420  
DB 389 GGTGCGACAGAAAGTATTTCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTT 448  
QY 421 GTGGGTGTACCGGACCGGATTTGAGACAGGTTTCAAGTGAAGTACTGTGAAGGGCT 480  
DB 449 GTGGGTGTACCGGACCGGATTTGAGACAGGTTTCAAGTGAAGTACTGTGAAGGGCT 508  
QY 481 TGTGCGACACAAAGAAATTTCCATTTTGTGCTACAGTCCAAAGAGTGAAGGACTGTGCT 540  
DB 509 TGTGCGACACAAAGAAATTTCCATTTTGTGCTACAGTCCAAAGAGTGAAGGACTGTGCT 568  
QY 541 CTGCGCAATGTGACTGCTATTTATTTTAACTTAACTTAACTTAACTTAACTTAACTT 600  
DB 569 CTGCGCAATGTGACTGCTATTTATTTTAACTTAACTTAACTTAACTTAACTTAACTT 628  
QY 601 AATCTGCTGTGAGAGGAAATGACAAATTAATTTGTTAGAGGAGGATTTGCAACCTGCT 660  
DB 629 AATCTGCTGTGAGAGGAAATGACAAATTAATTTGTTAGAGGAGGATTTGCAACCTGCT 688  
QY 661 GTGCAAAAGCTTTGAAAAAGAAAGAAAGATCCAAAGCTTGTGCTGCTGCTGCTGCT 720  
DB 689 GTGCAAAAGCTTTGAAAAAGAAAGAAAGATCCAAAGCTTGTGCTGCTGCTGCTGCT 748  
QY 721 GGAATAATTCGAAAGAAAGCAATTTTAACTTTTAACTTAACTTAACTTAACTTAACTT 780  
DB 749 GGAATAATTCGAAAGAAAGCAATTTTAACTTTTAACTTAACTTAACTTAACTTAACTT 808  
QY 781 GCTTATTTGCTTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTT 840  
DB 809 GCTTATTTGCTTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTT 868  
QY 841 TTGGTGAATTTATTCACAGTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTT 900  
DB 869 TTGGTGAATTTATTCACAGTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTT 928  
QY 901 TTTAATATTAATTAAGTCTGCTATTTCAAAATGAGTCTTACCAATTTTAACTTAACTTAACTT 960  
DB 929 TTTAATATTAATTAAGTCTGCTATTTCAAAATGAGTCTTACCAATTTTAACTTAACTTAACTT 988  
QY 961 TGTGTTGAGACTGAATTC 979  
DB 989 TGTGTTGAGACTGAATTC 1007

RESULT 7  
CR615468 1031 bp mRNA linear HTC 21-JUN-2004  
LOCUS full-length cDNA clone CS0D1068Y03 of Placenta Cot 25-normalized  
DEFINITION  
ACCESSION CR615468  
VERSION CR615468.1 GI:50496275  
KEYWORDS HTC, CNSLT, cDNA.  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE 1 (bases 1 to 1031)  
AUTHORS Li, W.B., Gruber, C., Jeesee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Paradise Avenue  
2 (bases 1 to 1031)  
REFERENCE  
AUTHORS Genoscope.  
TITLES Direct Submision  
JOURNAL Submitted (20-JUN-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr)  
COMMENT  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
FEATURES  
source location/Qualifiers  
1..1031  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0D1068Y03"  
/cissue\_type="Placenta Cot 25-normalized"  
/plasmid="pCMVSPORT\_6"  
ORIGIN  
Query Match 99.8%; Score 977.4; DB 4; Length 1031;  
Best Local Similarity 99.9%; Pred. No. 1.6e-243;  
Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GAGAGCCTTGGCCAGCGGGGCGCCGACCCCTGACACATGAGACCCGCTGCGCCCTTGG 60  
DB 17 GAGAGCCTTGGCCAGCGGGGCGCCGACCCCTGACACATGAGACCCGCTGCGCCCTTGG 76  
QY 61 GCGTGTGCAATTTCTGCTTTTCTGACAGAGGCTGCACTGGGCGATGTGCTCTCAAGAC 120  
DB 77 GCGTGTGCAATTTCTGCTTTTCTGACAGAGGCTGCACTGGGCGATGTGCTCTCAAGAC 136  
QY 121 CAACAGAAATTAACGCGAGATCTGCTCCGCCCTGAGCTAGAGGACCTGCGGGGCC 180  
DB 137 CAACAGAAATTAACGCGAGATCTGCTCCGCCCTGAGCTAGAGGACCTGCGGGGCC 196  
QY 181 TACTTCTCCGTTACTACGACAGGTACACGACAGCTGCGCCAGTTCCTGTACGGGG 240  
DB 197 TACTTCTCCGTTACTACGACAGGTACACGACAGCTGCGCCAGTTCCTGTACGGGG 256  
QY 241 GGTGCGAGGCGAAGCCCAATTTTCACTTCTGAGAGCTTGGGACATGTGCTGCTGGA 300  
DB 257 GGTGCGAGGCGAAGCCCAATTTTCACTTCTGAGAGCTTGGGACATGTGCTGCTGGA 316  
QY 301 GGATGAGAAAAAGTTCCCAAGTTTGGCGGTGCAAGTGTGAGAGGACGACAGTGTGAGG 360  
DB 317 GGATGAGAAAAAGTTCCCAAGTTTGGCGGTGCAAGTGTGAGAGGACGACAGTGTGAGG 376  
QY 361 GGTGCGACAGAAAGTATTTCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTT 420  
DB 377 GGTGCGACAGAAAGTATTTCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTT 436  
QY 421 GTGGGTGTACCGGACCGGATTTGAGACAGGTTTCCAGATGAAGCTACTGTGATGGCT 480  
DB 437 GTGGGTGTACCGGACCGGATTTGAGACAGGTTTCCAGATGAAGCTACTGTGATGGCT 496  
QY 481 TGTGCGACACAAAGAAATTTCCATTTTGTGCTACAGTCCAAAGAGTGAAGGACTGTGCT 540  
DB 497 TGTGCGACACAAAGAAATTTCCATTTTGTGCTACAGTCCAAAGAGTGAAGGACTGTGCT 556  
QY 541 CTGCGCAATGTGACTGCTATTTAATTTAATCCAGATACAGAACTGTGATGCTTCACT 600  
DB 557 CTGCGCAATGTGACTGCTATTTAATTTAATCCAGATACAGAACTGTGATGCTTCACT 616  
QY 601 AATCTGCTGTGAGAGGAAATGACAAATTAATTTGTTAGAGGAGAGATTGCAACCTGCTAT 660  
DB 617 AATCTGCTGTGAGAGGAAATGACAAATTAATTTGTTAGAGGAGAGATTGCAACCTGCTAT 676

QY 661 GNGCAAAAGCTTGAAGAAAGAAAGATGCAAGCTTGGCTTGGCAGTAGAATCC 720  
 DB 677 GGGCAAAAGCTTGAAGAAAGAAAGATGCAAGCTTGGCTTGGCAGTAGAATCC 736  
 QY 721 GGAATAATTCGGAAGAGCAATTTAAACATTTATATATGTCATCTTGTGCTTAAAG 780  
 DB 737 GGAATAATTCGGAAGAGCAATTTAAACATTTATATATGTCATCTTGTGCTTAAAG 796  
 QY 781 GCTTATTTGCTTATGTTGTTATCTGAAGAAATATATATGACAGCATGAGAAACAAATCA 840  
 DB 797 GCTTATTTGCTTATGTTGTTATCTGAAGAAATATATATGACAGCATGAGAAACAAATCA 856  
 QY 841 TTGGGATTTATTCACCGAGTTTATTTATATACAGCATCTTTTCAAAATTTGATTT 900  
 DB 857 TTGGGATTTATTCACCGAGTTTATTTATATACAGCATCTTTTCAAAATTTGATTT 916  
 QY 901 TTTATATATATACAGCTGCTATTCAAATGATGATACCATTTTAAATTTATGTTCAAC 960  
 DB 917 TTTATATATATACAGCTGCTATTCAAATGATGATACCATTTTAAATTTATGTTCAAC 976  
 QY 961 TGTTTGTGAGACTGAATTC 979  
 DB 977 TGTTTGTGAGACTGAATTC 995

## RESULT 8

CR612082 1033 bp mRNA linear HTC 21-JUL-2004  
 LOCUS full-length cDNA clone CS0D1012YJ24 of Placenta Cot 25-normalized  
 DEFINITION of Homo sapiens (human).

ACCESSION CR612082  
 VERSION CR612082.1 GI:50492889  
 KEYWORDS HTC; CDS; cDNA.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1033)  
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished  
 CONTACT : Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Faraday Avenue  
 2 (bases 1 to 1033)  
 REFERENCE Genoscope.  
 AUTHORS Direct Submision  
 TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
 JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen.  
 FEATURES Location/Qualifiers  
 source 1..1033  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS0D1012YJ24"  
 /issue\_type="Placenta Cot 25-normalized"  
 /plasmid="pCMVSPORT\_6"

## ORIGIN

Query Match 99.8%; Score 977.4; DB 4; Length 1033;  
 Best Local Similarity 99.8%; Pred. No. 1.6e-243;  
 Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 1 GGACGCTTGGCCAGCGGCGGCGGCGGCGGCTGACACATGAGACCCGCTGCGCCCTGCG 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 32 GGAAGCCTTGGCCAGCGGCGGCGGCGGCGGCTGACACATGAGACCCGCTGCGCCCTGCG 91  
 QY 61 GGGTGTGCAATTCGTGCTTTTCCGACGAGGCGTGCATGCGGCGGATGCTGTGTCAGAGC 120  
 DB 92 GGGTGTGCAATTCGTGCTTTTCCGACGAGGCGTGCATGCGGCGGATGCTGTGTCAGAGC 151  
 QY 121 CAACAGAAATTAACCGAGAGATCTGTCTCTGCCCCCTAGACTACGAGACCTTCCGCGGCC 180  
 DB 132 CAACAGAAATTAACCGAGAGATCTGTCTCTGCCCCCTAGACTACGAGACCTTCCGCGGCC 211  
 QY 181 TACTTCTCCGTTACTACTACGAGATACGAGAGAGTCCGCACTTCTGTACGCGG 240  
 DB 212 TACTTCTCCGTTACTACTACGAGATACGAGAGAGTCCGCACTTCTGTACGCGG 271  
 QY 241 GGTGGAAGGCAAGCCCAAAATTTCTACCTGTGAGGCTTGGAGATGCTGTGCGA 300  
 DB 272 GGTGGAAGGCAAGCCCAAAATTTCTACCTGTGAGGCTTGGAGATGCTGTGCGA 331  
 QY 301 GGAATGAAAAAGTTCCCAAGTTTCCGAGTGCAGAGATGATGAGACGACAGTGTGAGG 360  
 DB 332 GGAATGAAAAAGTTCCCAAGTTTCCGAGTGCAGAGATGATGAGACGACAGTGTGAGG 391  
 QY 361 GGTGCAAGAAAAATTAATTTCTTAATCTAAGTTCATGACATGTGAAAAATTTCTTTCG 420  
 DB 392 GGTGCAAGAAAAATTAATTTCTTAATCTAAGTTCATGACATGTGAAAAATTTCTTTCG 451  
 QY 421 GGTGTTGTCACCGGAAACCGGATTTGAGACAGTTTCCAGATGAACTCTGTATGAGGCT 480  
 DB 452 GGTGTTGTCACCGGAAACCGGATTTGAGACAGTTTCCAGATGAACTCTGTATGAGGCT 511  
 QY 481 TCTGGGCAACAAAGAAATTTCCATCATTTTGTCTACAGTCCAAAGATGAGGAGCTGTCT 540  
 DB 512 TCTGGGCAACAAAGAAATTTCCATCATTTTGTCTACAGTCCAAAGATGAGGAGCTGTCT 571  
 QY 541 CTGCCAATGTGACTGCTATTAATTTAAATCCAGATACAGAACTGTGATGCTTTCACCT 600  
 DB 572 CTGCCAATGTGACTGCTATTAATTTAAATCCAGATACAGAACTGTGATGCTTTCACCT 631  
 QY 601 ATACTGCTGTGAGAGGAAATGACATTAATTTGTTAGCAGGAGAGATTTGCCAAACGTGCAT 660  
 DB 632 ATACTGCTGTGAGAGGAAATGACATTAATTTGTTAGCAGGAGAGATTTGCCAAACGTGCAT 691  
 QY 661 GNGCAAAAGCTTGAAGAAAGAAAGATGCAAGCTTGGCTTGGCAGTAGAATCC 720  
 DB 692 GNGCAAAAGCTTGAAGAAAGAAAGATGCAAGCTTGGCTTGGCAGTAGAATCC 751  
 QY 721 GGAATAATTCGGAAGAGCAATTTAAACATTTATATATGTCATCTTGTGCTTAAAG 780  
 DB 752 GGAATAATTCGGAAGAGCAATTTAAACATTTATATATGTCATCTTGTGCTTAAAG 811  
 QY 781 GCTTATTTGCTTATGTTGTTATCTGAAGAAATATATATGACAGCATGAGAAACAAATCA 840  
 DB 812 GCTTATTTGCTTATGTTGTTATCTGAAGAAATATATATGACAGCATGAGAAACAAATCA 871  
 QY 841 TTGGGATTTATTCACCGAGTTTATTTATATACAGCATCTTTTCAAAATTTGATTT 900  
 DB 872 TTGGGATTTATTCACCGAGTTTATTTATATACAGCATCTTTTCAAAATTTGATTT 931  
 QY 901 TTTATATATATACAGCTGCTATTCAAATGATGATACCATTTTAAATTTATGTTCAAC 960  
 DB 932 TTTATATATATACAGCTGCTATTCAAATGATGATACCATTTTAAATTTATGTTCAAC 991  
 QY 961 TGTTTGTGAGACTGAATTC 979  
 DB 992 TGTTTGTGAGACTGAATTC 1010

## RESULT 9

CR601201 1034 bp mRNA linear HTC 21-JUL-2004  
 LOCUS full-length cDNA clone CS0D1075YM02 of Placenta Cot 25-normalized  
 DEFINITION of Homo sapiens (human).  
 ACCESSION CR601201

VERSION	CR601201.1	GI:50482008
KEYWORDS	HTC; CNSLT_cDNA.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.	
AUTHORS	1 (bases 1 to 1034)	
TITLE	LI, W.B., Gruber, C., Jesssee, J. and Polayes, D.	
JOURNAL	Full-length cDNA libraries and normalization	
REMARK	Unpublished	
COMMENT	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Paraday Avenue	
REFERENCE	2 (bases 1 to 1034)	
AUTHORS	Genoscope.	
TITLE	Direct Submision	
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr	
FEATURES	- Web : www.genoscope.cns.fr)	
FEATURES	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primers end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen	
FEATURES	Location/Qualifiers	
FEATURES	1..1034	
FEATURES	/organism="Homo sapiens"	
FEATURES	/mol_type="mRNA"	
FEATURES	/db_xref="taxon:9606"	
FEATURES	/clone="CS0D1075YM02"	
FEATURES	/issue_type="Placenta Cot 25-normalized"	
FEATURES	/plasmid="pCMVSPORT_6"	
ORIGIN		
Query Match	99.8%; Score 977.4; DB 4; Length 1034;	
Best Local Similarity	99.9%; Pred. No. 1.6e-243;	
Matches 978; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
Dy	1	GAAGCGCTTGGCCAGCGGCGCGCCCGACCCCTGTGACCATGAGACCCCGCTCGCCCTCTG 60
Db	37	GGAAGCCTTGGCCAGCGGCGCGCCCGACCCCTGTGACCATGAGACCCCGCTCGCCCTCTG 96
Dy	61	GCGTGTGATTTCTGCTGCTTTTCTGTACGAGGCTGCACTG3GCGATGCTCTCAAGAC 120
Db	97	GCGTGTGATTTCTGCTGCTTTTCTGTACGAGGCTGCACTG3GCGATGCTCTCAAGAC 156
Dy	121	CAACAGGAAATTAAGCGCGAGATCTGTCTCGGCCCTGTACGAGACCTCGCGCGGCC 180
Db	157	CAACAGGAAATTAAGCGCGAGATCTGTCTCGGCCCTGTACGAGACCTCGCGCGGCC 216
Dy	181	TACTTCTCCGTACTACTACGACAGGTACACGACAGAGCTGCGCAGTTCCTGTACGGG 240
Db	217	TACTTCTCCGTACTACTACGACAGGTACACGACAGAGCTGCGCAGTTCCTGTACGGG 276
Dy	241	GCTGCGAGGGCAAGCGCAATTTCTACCTTGAGAGCTTGGCGAGCTTGTCTG 300
Db	277	GCTGCGAGGGCAAGCGCAATTTCTACCTTGAGAGCTTGGCGAGCTTGTCTG 336
Dy	301	GGATTAAGAAAGTTCCCAAGTTTGGCGGCGTGAAGTGAAGTGAAGCAAGTGAAG 360
Db	337	GGATTAAGAAAGTTCCCAAGTTTGGCGGCGTGAAGTGAAGTGAAGCAAGTGAAG 396
Dy	361	GGTCCACAGAAAGTATTTCTTAACTTAATCTAAGTTCCATGACATGTGAATAATCTTTTCCG 420
Db	397	GGTCCACAGAAAGTATTTCTTAACTTAATCTAAGTTCCATGACATGTGAATAATCTTTTCCG 456
Dy	421	GTGGGTGTCAACCGGAACCGATTGAAGACAGGTTTCCAGATGAAGCTATGTATGGGCT 480
Db	457	GTGGGTGTCAACCGGAACCGATTGAAGACAGGTTTCCAGATGAAGCTATGTATGGGCT 516
Dy	481	TCTGCGCACCAAGAAATTCATCATTTTGTCTACAGTCCAAAGATGAAGGACATGTGCT 540

Db	517	TCGTGGCAGCAAAAGAAATTCATTCATTTTGCTGACATCCAAAGAGTAGGAGCATGTCCT	576
Oy	541	CTGCGCAATGTGACTCGCTATTATTATTCACAGATACAGAACTGTGATGCTTCACTT	600
Db	577	CTGCCAATGTGACACGCTATTATTATTCACAGATACAGAACTGTGATGCTTCACTT	636
Oy	601	ATACTGGCTGTGGAGGGAAATGACATTAATCTTTGTACAGAGGAGATTTGCAGAACTGCAT	660
Db	637	ATACTGGCTGTGGAGGGAAATGACATTAATCTTTGTACAGAGGAGATTTGCAGAACTGCAT	696
Oy	661	GTGCAAAAGCTTTGANAAGAAAAGAAAGATGCGCAAGCTTCGCTTGGCCAGTAGAATCC	720
Db	697	GTGCAAAAGCTTTGANAAGAAAAGAAAGATGCGCAAGCTTCGCTTGGCCAGTAGAATCC	756
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Db	757	GGAATAATTCGAGAGAGCAATTTTAAACATTTCTTAATATGTCAATCTTGTGCTTTATG	816
Oy	781	GCTAATTTGCTTTATGTTATGTTATGTAATCTGAAGAAATTAATGACAGATGAGAAACAATCA	840
Db	817	GCTAATTTGCTTTATGTTATGTTATGTAATCTGAAGAAATTAATGACAGATGAGAAACAATCA	876
Oy	841	TTGCTGATTTTATTCACGAGTTTATTTATTAATCAAGTCACTTTTCAAAAATTTGATTTT	900
Db	877	TTGCTGATTTTATTCACGAGTTTATTTATTAATCAAGTCACTTTTAAABAAATTTGATTTT	936
Oy	901	TTTATATATTAATCTAGCTGCTATTTCAAATGTGAGTCTACATTTTAAATTTATGTTCAC	960
Db	937	TTTATATATTAATCTAGCTGCTATTTCAAATGTGAGTCTACATTTTAAATTTATGTTCAC	996
Oy	961	TGTTTGTGAGCTGGAATTC 979	
Db	997	TGTTTGTGAGCTGGAATTC 1015	
RESULT 10			
LOCUS	CR618958		
DEFINITION	full-length cDNA clone CSOD1058Y18 of Placenta Cot 25-normalized		
ACCESSION	CR618958		
VERSION	CR618958.1		
KEYWORDS	HTC; CNSIT_cDNA.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Bukacynski; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 (bases 1 to 1038)		
TITLE	L1,W.B., Gruber,C., Jesses,J. and Polayes,D.		
JOURNAL	Full-length cDNA libraries and normalization		
REMARK	Unpublished		
	Contact : Feng Liang Email : fliang@life.techn.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600		
REFERENCE	2 (bases 1 to 1038)		
AUTHORS	Paradey Avenue		
TITLE	Genoscope.		
JOURNAL	Direct Submission		
	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segret@genoscope.cns.fr		
COMMENT	- Web : www.genoscope.cns.fr)		
	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primers		
	end enriched, double-strand cDNA was digested with Not I and cloned		
	into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library		
	was normalized. Library was constructed by Life Technologies, a		
	division of Invitrogen.		
FEATURES	Location/Qualifiers		
source	1..1038		
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	/mol_type="RNA"		
	/db_xref="taxon:9606"		
	/clone="CSOD1058Y18"		
	/tissue="Placenta Cot 25-normalized"		





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Qy 421 GTGGGTGTACCGGAAACCGGATTTGAGAACAGTTTCCAGTGAAGTACTGTATGGGCT 480  
Db 449 GTGGGTGTACCGGAAACCGGATTTGAGAACAGTTTCCAGTGAAGTACTGTATGGGCT 508  
Qy 481 TCTGGCAGCCAAAGAAATTCATCTTTTCTCAAGTCCAAAAGATGAGGAGCTGTGCT 540  
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Qy 541 CTGGCAATGATGCTGCTATTTATTTAATCCAGATGAGAACCTGTGATGCTTTCACCT 600  
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Db 629 ATACTGCTGTGGAGGGAATGACATATACCTTTGTAGCAGGAGATTCGCAACGTGCAT 688  
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Db 689 GTGCAAAAGCTTTGAAAAAGAAAGAGATGCAAGCTTGTGCTGCAAGATCC 748  
Qy 721 GGAATAATTTGGAAGAGCAATTTTAACTCTTAATATGTCATCTTTGTGCTTATG 780  
Db 749 GGAATAATTTGGAAGAGCAATTTTAACTCTTAATATGTCATCTTTGTGCTTATG 808  
Qy 781 GCTATTTGCTTTATGTTGTATCTGAAGAAATATATGACAGATGAGAAACAAATCA 840  
Db 809 GCTATTTGCTTTATGTTGTATCTGAAGAAATATATGACAGATGAGAAACAAATCA 868  
Qy 841 TTGGTGATTTATTCACCAAGTTTATTAATACAGTCACTTTTCAAAAATTTGATTT 900  
Db 869 TTGGTGATTTATTCACCAAGTTTATTAATACAGTCACTTTTCAAAAATTTGATTT 928  
Qy 901 TTATATATATATAGTGTATTTCAAAATGAGTCAAGTATTTATTTATTTATGTTCAAC 960  
Db 929 TTATATATATATAGTGTATTTCAAAATGAGTCAAGTATTTATTTATTTATGTTCAAC 988  
Qy 961 TGTGTGTGAGACTGAATTC 979  
Db 989 TGTGTGTGAGACTGAATTC 1007

RESULT 12  
CR621074 1042 bp mRNA linear HTC 21-JUL-2004  
LOCUS Full-length cDNA clone CS0D1012YA05 of Placenta Cot 25-normalized  
DEFINITION CR621074  
ACCESSION CR621074  
VERSION CR621074.1 GI:50501881  
KEYWORDS HTC; CNSLT CDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
1 (bases 1 to 1042)  
REFERENCE 1 (bases 1 to 1042)  
AUTHORS Li W.B., Gruber C., Jessee J. and Polayes D.  
JOURNAL Full-length cDNA libraries and normalization  
REMARK Unpublished  
Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Paradise Avenue  
2 (bases 1 to 1042)  
REFERENCE Genoscope.  
AUTHORS Direct Submision  
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
FEATURES  
Location/Qualifiers  
source 1..1042  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0D1012YA05"  
/tissue\_type="Placenta Cot 25-normalized"  
/plasmid="pCMVSPORT\_6"

Query Match 99.8%; Score 977.4; DB 4; Length 1042;  
Best Local Similarity 99.9%; Pred. No. 1.6e-243;  
Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 GGAGCCCTTGGCCAGCGGCGCCGACCCCTGACATGAGACCCCGTGGCCCGCC 60  
Db 37 GGAGCCCTTGGCCAGCGGCGCCGACCCCTGACATGAGACCCCGTGGCCCGCC 96  
Qy 61 GGCTGTGATTTCTGTGCTTTTCTGACGAGGCTGCACTGGGCGATGCTGCTCAGAGC 120  
Db 97 GGCTGTGATTTCTGTGCTTTTCTGACGAGGCTGCACTGGGCGATGCTGCTCAGAGC 156  
Qy 121 CAACAGAAATPACGCGAGATCTGTCTCTGCCCCCTAGACTAGCGACCTTCCGCGCC 180  
Db 157 CAACAGAAATPACGCGAGATCTGTCTCTGCCCCCTAGACTAGCGACCTTCCGCGCC 216  
Qy 181 TACTTCTCCGTACTACATACAGATACAGGATACAGGAGTCCGACGTTCCGTACGCGG 240  
Db 217 TACTTCTCCGTACTACATACAGATACAGGATACAGGAGTCCGACGTTCCGTACGCGG 276  
Qy 241 GCTGCGAGGCAACGCAACATTTCTACACCTGGAGGCTTGCAGCATGCTTCTGGA 300  
Db 277 GCTGCGAGGCAACGCAACATTTCTACACCTGGAGGCTTGCAGCATGCTTCTGGA 336  
Qy 301 GGATGAAAAAGTTCCCAAGTTTCCGCGCTGCAAGTGAAGTGAACAACATGTGAGG 360  
Db 337 GGATGAAAAAGTTCCCAAGTTTCCGCGCTGCAAGTGAAGTGAACAACATGTGAGG 396  
Qy 361 GGTCCAGAAAAAGTATTTCTTTAATCAAGTCCATGACATGAGAAAAATTTCTTTCCG 420  
Db 397 GGTCCAGAAAAAGTATTTCTTTAATCAAGTCCATGACATGAGAAAAATTTCTTTCCG 456  
Qy 421 GTGGGTGTACCGGAAACCGGATTTGAGAACAGTTTCCAGTGAAGTACTGTATGGGCT 480  
Db 457 GTGGGTGTACCGGAAACCGGATTTGAGAACAGTTTCCAGTGAAGTACTGTATGGGCT 516  
Qy 481 TCTGGCAGCCAAAGAAATTCATCTTTTCTCAAGTCCAAAAGATGAGGAGCTGTGCT 540  
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Qy 721 GGAATAATTTGGAAGAGCAATTTTAACTCTTAATATGTCATCTTTGTGCTTATG 780  
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Qy 781 GCTATTTGCTTTATGTTGTATCTGAAGAAATATATGACAGATGAGAAACAAATCA 840  
Db 817 GCTATTTGCTTTATGTTGTATCTGAAGAAATATATGACAGATGAGAAACAAATCA 876  
Qy 841 TTGGTGATTTATTCACCAAGTTTATTAATACAGTCACTTTTCAAAAATTTGATTT 900



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Db 877 TTGGATTATTCACCAAGTTTATATACAGTCTTTAAAAATTGATTT 936  
Qy 901 TTTATATTAATCTACTGTATTTAAATGTAGTCTACATTTTATATATGTTTCAAC 960  
Db 937 TTTATATTAATCTACTGTATTTAAATGTAGTCTACATTTTATATGTTTCAAC 996  
Qy 961 TGTGTGAGACTGAATTC 979  
Db 997 TGTGTGAGACTGAATTC 1015

RESULT 13  
CR611856 1046 bp mRNA linear HTC 21-JUL-2004  
LOCUS full-length cDNA clone CS0D1073YH22 of Placenta Cot 25-normalized  
DEFINITION  
ACCESSION CR611856  
VERSION CR611856.1 GI:50492663  
KEYWORDS HTC; CNSLT cDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE 1 (bases 1 to 1046)  
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Paradey Avenue  
2 (bases 1 to 1046)  
REFERENCE  
AUTHORS Direct Submision  
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr  
COMMENT - Web : www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
FEATURES  
source location/Qualifiers  
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ORIGIN  
Query Match 99.8%; Score 977.4; DB 4; Length 1046;  
Best Local Similarity 99.9%; Pred No. 1.6e-243;  
Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAGCGCTTGGCCAGCGGGCGCCGACCCCTGACATGACCCCGCTCGCCCTTGG 60  
Db 32 GGAGCGCTTGGCCAGCGGGCGCCGACCCCTGACATGACCCCGCTCGCCCTTGG 91  
Qy 61 GGCTGTGATTTCTGCTGCTTTTCTGACGAGAGCTGCACTGGGGCGATGCTGCTCAGAGAC 120  
Db 92 GGCTGTGATTTCTGCTGCTTTTCTGACGAGAGCTGCACTGGGGCGATGCTGCTCAGAGAC 151  
Qy 121 CAACGAGAAATACGCGAGATCTGCTCTGCGCCCTAAGTACGAGACCTGCGGGGCC 180  
Db 132 CAACGAGAAATACGCGAGATCTGCTCTGCGCCCTAAGTACGAGACCTGCGGGGCC 211  
Qy 181 TACTTCTCCGTTACTACTACGACAGGTACACGAGAGCTGCGCGAGTTCTGTACGGGG 240  
Db 212 TACTTCTCCGTTACTACTACGACAGGTACACGAGAGCTGCGCGAGTTCTGTACGGGG 271

Qy 241 GCTGCGAGGGCAACGCCAATTTCTACACTTGGAGGCTTGGCAGATCTTGCTGGA 300  
Db 272 GCTGCGAGGGCAACGCCAATTTCTACACTTGGAGGCTTGGCAGATCTTGCTGGA 331  
Qy 301 GGATGAGAAAAAGTTTCCCAAGTTTGGCGCTGCAAGTATGTGAGACACAGTGTAGG 360  
Db 332 GGATGAGAAAAAGTTTCCCAAGTTTGGCGCTGCAAGTATGTGAGACACAGTGTAGG 391  
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Qy 421 GTGGGTGTACCCGGAACCGAATGAGACAGATTTCCAGATGAACTTGTATGGCT 480  
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Qy 481 TCTGCGCACCAAGAAAAATTCATCATTTTGTCTACAGTCCAAAGATGAGGACTGTGCT 540  
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Qy 781 GCTAATTTGCTTTATGTTGATCTGAAGATATATATGACAGATGAGAAAAATCA 840  
Db 812 GCTAATTTGCTTTATGTTGATCTGAAGATATATATGACAGATGAGAAAAATCA 871  
Qy 841 TTGGTATTTATTCACAGATTTTATTAATACAGTCACTTTTCAAAAAATTTGATTT 900  
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Qy 961 TGTGTGAGACTGAATTC 979  
Db 992 TGTGTGAGACTGAATTC 1010

RESULT 14  
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LOCUS full-length cDNA clone CS0D1075YH17 of Placenta Cot 25-normalized  
DEFINITION  
ACCESSION CR605333  
VERSION CR605333.1 GI:50486140  
KEYWORDS HTC; CNSLT cDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE 1 (bases 1 to 1047)  
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Paradey Avenue

REFERENCE 2 (bases 1 to 1047)  
 AUTHORS Genoscope.  
 TITLE Direct Submission  
 JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.  
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 Query Match 99.8%; Score 977.4; DB 4; Length 1047;  
 Best Local Similarity 99.9%; Pred. No. 1.6e-243;  
 Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 1 GAAGCGCTTGGCCAGCGGCGCCGCCGACCCCTGACACATGACCCCGCTGCGCCCTGG 60  
 29 GAGCGCTTGGCCAGCGGCGCCGCCGACCCCTGACACATGACCCCGCTGCGCCCTGG 88  
 61 GGCTGTGCAATTCGCTGCTTTCTGACGAGGCTGCACTGGGGCATGCTGCTGACAGC 120  
 89 GGCTGTGCAATTCGCTGCTTTCTGACGAGGCTGCACTGGGGCATGCTGCTGACAGC 148  
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 209 TACTTCTCCGTTACTACTACGAGGTACGAGGTGCGCGGCAAGTTCTGTACGAGG 268  
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 629 ATACTGCTGTGAGGGAATGACATTAATTTGTTTGAAGGAGGAGATTGCAAACTGCAAT 688  
 661 GTGCAAAAGCTTTGAAAAAGAAAGATGCAAAAGCTTGTGCTTGTGCAATGAAATCC 720  
 689 GTGCAAAAGCTTTGAAAAAGAAAGATGCAAAAGCTTGTGCTTGTGCAATGAAATCC 748

721 GAAAAATCGAAGAGCAATTTTAAAGTCTTAATATGACATGCTGTTGCTTTATG 780  
 749 GAAAAATCGAAGAGCAATTTTAAAGTCTTAATATGACATGCTGTTGCTTTATG 808  
 781 GCTTATTTGCCCTTATGTTGATCTGAAGATATATATGACATGAGAGAAACAATCA 840  
 809 GCTTATTTGCCCTTATGTTGATCTGAAGATATATATGACATGAGAGAAACAATCA 868  
 841 TTGGTATTTATTCACAGTTTATTTATTAACAAGTCACTTTTCAAAAATTTGGATTTT 900  
 869 TTGGTATTTATTCACAGTTTATTTATTAACAAGTCACTTTTCAAAAATTTGGATTTT 928  
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 929 TTTATATATTAACCTAGCTGCTTATTAAGATGAGCTTACATTTTATTTATGTTTCAAC 988  
 961 TGTGTTGAGACTGAATTC 979  
 989 TGTGTTGAGACTGAATTC 1007  
 RESULT 15  
 CR607266 1050 bp mRNA linear HTC 21-JUL-2004  
 LOCUS Full-length cDNA clone CSOD1067A08 of Placenta Cot 25-normalized  
 DEFINITION of Homo sapiens (human).  
 ACCESSION CR607266  
 VERSION CR607266.1 GI:50488073  
 KEYWORDS HTC; CNSLT cDNA.  
 SOURCE  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1050)  
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished  
 CONTACT : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue  
 2 (bases 1 to 1050)  
 REFERENCE Genoscope.  
 AUTHORS Direct Submission  
 TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr  
 COMMENT - Web : www.genoscope.cns.fr)  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.  
 FEATURES  
 source location/Qualifiers  
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 /db\_xref="taxon:9606"  
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 /plasmid="pCMVSPORT\_6"  
 ORIGIN  
 Query Match 99.8%; Score 977.4; DB 4; Length 1050;  
 Best Local Similarity 99.9%; Pred. No. 1.6e-243;  
 Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 1 GAAGCGCTTGGCCAGCGGCGCCGCCGACCCCTGACACATGACCCCGCTGCGCCCTGG 60  
 36 GAGCGCTTGGCCAGCGGCGCCGCCGACCCCTGACACATGACCCCGCTGCGCCCTGG 95  
 61 GGCTGTGCAATTCGCTGCTTTCTGACGAGGCTGCACTGGGGCATGCTGCTGACAGC 120  
 96 GGCTGTGCAATTCGCTGCTTTCTGACGAGGCTGCACTGGGGCATGCTGCTGACAGC 155

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DB 156 CAACAGAAATACCGGAGATCTGTCTGCCCCCTAGACTACGGAACCTGCGGGGCC 215
QY 181 TACTTCTCCGTTACTACTACGACAGGTACACGCAAGCTGCGCCAGTTCTGTACGGGG 240
DB 216 TACTTCTCCGTTACTACTACGACAGGTACACGCAAGCTGCGCCAGTTCTGTACGGGG 275
QY 241 GCTGCGAGGGCAACGCGCAACATTTTACACCTGGAGGCTTGCACAGATGCTTGTGGA 300
DB 276 GCTGCGAGGGCAACGCGCAACATTTTACACCTGGAGGCTTGCACAGATGCTTGTGGA 335
QY 301 GGAATGAAAAAGTTCCCAAGTTGCGGCTGCAAGTGAAGTGAAGCAAGTGAAG 360
DB 336 GGAATGAAAAAGTTCCCAAGTTGCGGCTGCAAGTGAAGTGAAGCAAGTGAAG 395
QY 361 GGTCCACAGAAAAATTTCTTAACTTAAGTTCATGACATGTGAAAAATCTTTCCG 420
DB 396 GGTCCACAGAAAAATTTCTTAACTTAAGTTCATGACATGTGAAAAATCTTTCCG 455
QY 421 GTGGGTGTACCGGAAACCGGATTTGAGACAGGTTTCCAGATGAAGCTACTGTATGGCT 480
DB 456 GTGGGTGTACCGGAAACCGGATTTGAGACAGGTTTCCAGATGAAGCTACTGTATGGCT 515
QY 481 TGTGGCACAAGAAAAATTTCAATCTTTTGTACAGTCCAAAAGATGAGGACGTGTCT 540
DB 516 TGTGGCACAAGAAAAATTTCAATCTTTTGTACAGTCCAAAAGATGAGGACGTGTCT 575
QY 541 CTGCCAATGTGACTCGCTATTATTTTAACTCAAGATACAGAACTGTGATGCTTCACT 600
DB 576 CTGCCAATGTGACTCGCTATTATTTTAACTCAAGATACAGAACTGTGATGCTTCACT 635
QY 601 AATCTGGCTGTGAGGGAATGACAAATACCTTTGTAGCAGGAGAAATGCAACGTGCAT 660
DB 636 AATCTGGCTGTGAGGGAATGACAAATACCTTTGTAGCAGGAGAAATGCAACGTGCAT 695
QY 661 GTGCAAAAAGCTTTGAAAAAGAAAAAGAAATGCCAAAGCTTGGCAATGAAATCC 720
DB 696 GTGCAAAAAGCTTTGAAAAAGAAAAAGAAATGCCAAAGCTTGGCAATGAAATCC 755
QY 721 GGAATAATCGAAGAAAGCAATTTTAAACATCTTAATATGTCATCTTGTGTCTTATG 780
DB 756 GGAATAATCGAAGAAAGCAATTTTAAACATCTTAATATGTCATCTTGTGTCTTATG 815
QY 781 GCTTATTTGCTTTATGTTGTTATCTGAAGAAATATATGACAGCATGAGGAAACAAATCA 840
DB 816 GCTTATTTGCTTTATGTTGTTATCTGAAGAAATATATGACAGCATGAGGAAACAAATCA 875
QY 841 TTGGTGATTTATTCACCAATTTTATTAATACAGTCACTTTTCAAAAATTTGATTTT 900
DB 876 TTGGTGATTTATTCACCAATTTTATTAATACAGTCACTTTTCAAAAATTTGATTTT 935
QY 901 TTTATATATACATAGCTGCTATTCAATGAGTACATTTTAAATTTAATGATGCAAC 960
DB 936 TTTATATATACATAGCTGCTATTCAATGAGTACATTTTAAATTTAATGATGCAAC 995
QY 961 TGTGTGAGACTGAATTC 979
DB 996 TGTGTGAGACTGAATTC 1014
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Search completed: March 11, 2006, 08:20:02  
Job time : 4768 secs

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NAME/KEY: CDS  
LOCATION: 39..746  
US-08-147-710-1

Query Match 100.0%; Score 979; DB 2; Length 979;  
Best Local Similarity 100.0%; Pred. No. 1.8e-264; Indels 0; Gaps 0;  
Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGCGCTTGGCCAGCGGGCGCCGACCCCTGACCAATGAGCCCGCTGCGCCCTGG 60  
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DB 121 CAACAGAAATTAACGGGAGATCTGCTCTGCGCCCTAGACTACGGAACCTGCGGGGCC 180  
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DB 541 CTGCGCAATGTGACTGCTATTAATTTTAATCCAAAGTACGAACTGTGATGCTTTCACCT 600  
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DB 601 ATACTGCTGTGAGGAGAAATTCATTAATTTTGAAGGAGGAGGAGGAGGAGGAGGAGG 660  
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DB 661 GTGCAAAAGCTTTGAAAAAGAAAAAGAAATGCAAAAGCTTGGCTTGGCAGTAGAATCC 720  
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DB 721 GGAATAATTCGAAAGAGCAATTTTAACATTTTAATATGATCATCTGTGTTGCTTTAAG 780  
QY 781 GCTTATTTGCTTTATGTTGATCTGAAGAAATTAATGAAGGAGGAGGAGGAGGAGGAGG 840  
DB 781 GCTTATTTGCTTTATGTTGATCTGAAGAAATTAATGAAGGAGGAGGAGGAGGAGGAGG 840  
QY 841 TTGGTGAATTAATTCAGATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 900  
DB 841 TTGGTGAATTAATTCAGATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 900  
QY 901 TTTATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 960  
DB 901 TTTATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 960  
QY 961 TGTGTTGAGACTGAATTC 979

DB 961 TGTGTTGAGACTGAATTC 979

RESULT 2  
US-08-458-090-1

Sequence 1, Application US/08458090  
Patent No. 5728674

GENERAL INFORMATION:  
APPLICANT: Sprecher, Cindy A.

APPLICANT: Kistler, Walter

APPLICANT: Foster, Donald C.

TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS AND

NUMBER OF SEQUENCES: 15  
METHODS RELATING THERETO

CORRESPONDENCE ADDRESS:  
ADDRESS: ZymoGenetics, Inc.

STREET: 1201 Baseline Avenue East

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98102

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458, 090

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:  
NAME: Parker, Gary B.

REGISTRATION NUMBER: 31-648

REFERENCE/DOCKET NUMBER: 93-14D2

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6673

TELEFAX: 206-442-6678

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 979 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

TISSUE TYPE: Placenta

IMMEDIATE SOURCE:

CLONE: J-2-11

FEATURES:

NAME/KEY: CDS

LOCATION: 39..746

US-08-458-090-1

Query Match 100.0%; Score 979; DB 2; Length 979;  
Best Local Similarity 100.0%; Pred. No. 1.8e-264; Indels 0; Gaps 0;  
Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGCGCTTGGCCAGCGGGCGCCGACCCCTGACCAATGAGCCCGCTGCGCCCTGG 60  
DB 1 GGAGGCGCTTGGCCAGCGGGCGCCGACCCCTGACCAATGAGCCCGCTGCGCCCTGG 60  
QY 61 GGCTGTGCAATTCCTGCTGCTTTCTGACGAGGCTGCACTGGGCGCATGCTGCTCAGAGC 120  
DB 61 GGCTGTGCAATTCCTGCTGCTTTCTGACGAGGCTGCACTGGGCGCATGCTGCTCAGAGC 120  
QY 121 CAACAGAAATTAACGGGAGATCTGCTCTGCGCCCTAGACTACGGAACCTGCGGGGCC 180  
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DB |||||  
QY 241 GCTGCGAGGGGCAACGCAAAATTTCTACCTGGAGGCTTTGGAGAGATGCTTGCTGGA 300  
DB |||||  
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DB 301 GGATGAGAAAAAGTTCCCAAGTTTCCCGGCTGCAAGTGAAGTGGACGACAGTGTGAG 360  
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DB 361 GGTCCACAGAAAAAGTATTTCTTAATCTAAGTTCCAGTACATGTGAAAAATTTCTTTCCG 420  
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DB 481 TCTGGGACCAAGAAAAATTCATCTTTTGTCTACAGTCCAAAAGATGAGGAGCTGTGCT 540  
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DB 541 CTGCGCAATGTGATCTGCTATTAATTTAAATCCAGATACAGAACTGTGATGCTTCACT 600  
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QY 721 GGAATAATTCGAGAGAGCAATTTAAATCTTAATATGTCATCTTGTGTCTTTAAG 780  
DB 721 GGAATAATTCGAGAGAGCAATTTAAATCTTAATATGTCATCTTGTGTCTTTAAG 780  
QY 781 GCTTATTTGCTTTATGTTGTTATCTGAAGATATATGACGATGAGGAGAAACAAATCA 840  
DB 781 GCTTATTTGCTTTATGTTGTTATCTGAAGATATATGACGATGAGGAGAAACAAATCA 840  
QY 841 TTGGGATTTATTCACAGTTTATTAATATACAGTCACTTTTCAAAAATTTGGAATTT 900  
DB 841 TTGGGATTTATTCACAGTTTATTAATATACAGTCACTTTTCAAAAATTTGGAATTT 900  
QY 901 TTTATATATTAAGTCTGATTAATCAATGTGAGTCTACATTTTAAATTAATGTTCAAC 960  
DB 901 TTTATATATTAAGTCTGATTAATCAATGTGAGTCTACATTTTAAATTAATGTTCAAC 960  
QY 961 TGTTTGTGAGACTGAATTC 979  
DB 961 TGTTTGTGAGACTGAATTC 979

RESULT 3  
US-08-457-887-1Sequence 1, Application US/08457887  
Patent No. 5914315

GENERAL INFORMATION:  
APPLICANT: Sprecher, Cindy A.  
APPLICANT: Kiesel, Walter  
APPLICANT: Foster, Donald C.  
TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS AND  
TITLE OF INVENTION: METHODS RELATING THEREIN  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Zymogenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/457,887  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, Gary E  
REGISTRATION NUMBER: 31-648  
REFERENCE/DOCKET NUMBER: 93-14D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6673  
TELEFAX: 206-442-6678  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 979 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
TISSUE TYPE: Placenta  
IMMEDIATE SOURCE:  
CLONE: J-2-11  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 39..746  
US-08-457-887-1

Query Match 100.0%; Score 979; DB 2; Length 979;  
Best Local Similarity 100.0%; Pred. No. 1,8e-264; Indels 0; Gaps 0;  
Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCGCTTGGCCGAGCGGCGCCGACCCCTGCAACCATGAGACCCCGCTGCGCCCTG 60  
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DB 301 GGATGAGAAAAAGTTCCCAAGTTTCCCGGCTGCAAGTGAAGTGGACGACAGTGTGAG 360  
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QY 541 CTGCCAATGCTGCTATTTATTTATTCAGATACGAACCTGTGATGCTTCACT 600  
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QY 661 GTGCAAAAGCTTTGAAAAAGAAAAAGAGATGCCAAAGCTTGTGCACTAGAAATCC 720  
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Db 841 TTGGTGAATTTATTCACAGTTTATTTATTAATACAGTCACTTTTCAAAATTTGATTT 900  
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QY 901 TTTATATATTAATTAAGTCTGATTTCAATGTGCTACCATTTTAAATTATGTTCAAC 960  
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Db 901 TTTATATATTAATTAAGTCTGATTTCAATGTGCTACCATTTTAAATTATGTTCAAC 960  
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QY 961 TGTGTGAGACTGAATTC 979  
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Db 961 TGTGTGAGACTGAATTC 979  
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## RESULT 4

US-09-016-434-1378

Sequence 1378 Application US/09016434

Patent No. 6500938

GENERAL INFORMATION:

APPLICANT: Janice Au-Young

APPLICANT: Jeffrey J. Selthamer

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

TITLE OF INVENTION: PATHWAY GENE EXPRESSION

NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/016.434

FILING DATE: HEREWITH

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0002 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1378:

SEQUENCE CHARACTERISTICS:

LENGTH: 979 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: 9441149  
US-09-016-434-1378

Query Match 100.0%; Score 979; DB 3; Length 979;  
Best Local Similarity 100.0%; Pred. No. 1,8e-264;  
Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGAGCTTCGCCAGCGGGCCGCCGACCCCTGACCAATGAGACCCGCTGCCCCCTGG 60  
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QY 661 GTGCAAAAGCTTTGAAAAAGAAAAAGAGATGCCAAAGCTTGTGCACTAGAAATCC 720  
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QY 781 GCTATTGCTTTATGCTGATCTGATGCAAGATTAATATGACAGCAAGGAAACAAATCA 840  
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QY 841 TTGGTGAATTTATTCACAGTTTATTTATTAATACAGTCACTTTTCAAAATTTGATTT 900  
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QY 901 TTTATATTAATTAAGTCTGATTTCAATGTGCTACCATTTTAAATTATGTTCAAC 960  
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Db 901 TTTATATATACAGCTGCTATTCGAATGATGATCTACATTTTAAATTATGTTCAAC 960  
Qy 961 TGTGTGAGACTGAATTC 979  
Db 961 TGTGTGAGACTGAATTC 979

## RESULT 5

US-09-904-621-1  
Sequence 1, Application US/09904621  
Patent No. 6656746  
GENERAL INFORMATION:  
APPLICANT: Sprecher, Cindy A.  
APPLICANT: Kistler, Walter  
APPLICANT: Foster, Donald C.  
TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS  
TITLE OF INVENTION: AND  
FILE REFERENCE: 93-14D3  
CURRENT APPLICATION NUMBER: US/09/904,621  
CURRENT FILING DATE: 2001-07-13  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/265,627  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 5,455,338  
PRIOR FILING DATE: EARLIER FILING DATE: 1993-11-05  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 979  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (39)...(746)  
US-09-904-621-1

Query Match 100.0%; Score 979; DB 3; Length 979;  
Best Local Similarity 100.0%; Pred. No. 1,86-264;  
Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGAGCCCTTGGCCAGCGGGCGCCGAGCCCTGTGACCATGAGACCCCGCTGCGCCCTGG 60  
Db 1 GAGAGCCCTTGGCCAGCGGGCGCCGAGCCCTGTGACCATGAGACCCCGCTGCGCCCTGG 60  
Qy 61 GAGTGTGATTCGTGCTGCTTTTCTGACGAGGCTGCACTGCGGAGTCTGCTGAGAGC 120  
Db 61 GAGTGTGATTCGTGCTGCTTTTCTGACGAGGCTGCACTGCGGAGTCTGCTGAGAGC 120  
Qy 121 CAACAGGAAATACGCGGAGATCTGCTGCTGCTGAGTACGAGACCTGCGGGGCC 180  
Db 121 CAACAGGAAATACGCGGAGATCTGCTGCTGCTGAGTACGAGACCTGCGGGGCC 180  
Qy 181 TACTTCTCGTACTACTACGACAGGTACAGGAGTGGCGGAGTTCGTTACGAGG 240  
Db 181 TACTTCTCGTACTACTACGACAGGTACAGGAGTGGCGGAGTTCGTTACGAGG 240  
Qy 241 GCTGCGAGGCAACGCAATTTCTACCTGTGAGGCTTGCAGACGATGCTTGTG 300  
Db 241 GCTGCGAGGCAACGCAATTTCTACCTGTGAGGCTTGCAGACGATGCTTGTG 300  
Qy 301 GATGAGAAAGTTTCCCAAGTTTCCGCGCTGCAAGTACGATGAGCAACGATGAG 360  
Db 301 GATGAGAAAGTTTCCCAAGTTTCCGCGCTGCAAGTACGATGAGCAACGATGAG 360  
Qy 361 GATGAGAAAGTTTCCCAAGTTTCCGCGCTGCAAGTACGATGAGCAACGATGAG 420  
Db 361 GATGAGAAAGTTTCCCAAGTTTCCGCGCTGCAAGTACGATGAGCAACGATGAG 420  
Qy 421 GTGGGTGTCAACGAGACCGGATGAGACAGGTTTCCAGATGAGACTCTGTATGAG 480  
Db 421 GTGGGTGTCAACGAGACCGGATGAGACAGGTTTCCAGATGAGACTCTGTATGAG 480

Qy 481 TCTGCGACCAAGAAATTCATCTATTTGCTACAGTCCAAAGATGAGGAGCTGCT 540  
Db 481 TCTGCGACCAAGAAATTCATCTATTTGCTACAGTCCAAAGATGAGGAGCTGCT 540  
Qy 541 CTGCGCAATGTGACTGCTATTTATTTATTCAGATACAGAACTGTGATCTTCACT 600  
Db 541 CTGCGCAATGTGACTGCTATTTATTTATTCAGATACAGAACTGTGATCTTCACT 600  
Qy 601 ATACTGCTGTGAGGAGAAATCAATTAATTTTACAGGAGAGATTTGCAAGTGAT 660  
Db 601 ATACTGCTGTGAGGAGAAATCAATTAATTTTACAGGAGAGATTTGCAAGTGAT 660  
Qy 661 GTGCAAAAGCTTTGAAAGAAAGAAAGATGCAAGCTTGTGCTGAGTAAATCC 720  
Db 661 GTGCAAAAGCTTTGAAAGAAAGAAAGATGCAAGCTTGTGCTGAGTAAATCC 720  
Qy 721 GAAATTCGAGAGACATTTTAAATTTTAAATTAATGATCTGTTGCTTATG 780  
Db 721 GAAATTCGAGAGACATTTTAAATTTTAAATTAATGATCTGTTGCTTATG 780  
Qy 781 GCTATTTGCTTTATGCTTATCTGATCTGAGATTAATATGACAGATGAGAAACAAATCA 840  
Db 781 GCTATTTGCTTTATGCTTATCTGATCTGAGATTAATATGACAGATGAGAAACAAATCA 840  
Qy 841 TTGGGATTTATTCACGAGTATTTATTAATCAAGTCACTTTTCAAAATTTGATTT 900  
Db 841 TTGGGATTTATTCACGAGTATTTATTAATCAAGTCACTTTTCAAAATTTGATTT 900  
Qy 901 TTTATATATACAGCTGCTATTTCAAAATGATGATCTACATTTTAAATTATGTTCAAC 960  
Db 901 TTTATATATACAGCTGCTATTTCAAAATGATGATCTACATTTTAAATTATGTTCAAC 960  
Qy 961 TGTGTGAGACTGAATTC 979  
Db 961 TGTGTGAGACTGAATTC 979

## RESULT 6

US-09-949-016-1187  
Sequence 1187, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CLO01307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1187  
LENGTH: 1583  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-1187

Query Match 99.8%; Score 977.4; DB 3; Length 1583;  
Best Local Similarity 99.9%; Pred. No. 6,4e-264;  
Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAGAGCCCTTGGCCAGCGGGCGCCGAGCCCTGTGACCATGAGACCCCGCTGCGCCCTGG 60  
Db 1 GAGAGCCCTTGGCCAGCGGGCGCCGAGCCCTGTGACCATGAGACCCCGCTGCGCCCTGG 60  
Qy 61 GAGTGTGATTCGTGCTGCTTTTCTGACGAGGCTGCACTGCGGAGTCTGCTGAGAGC 120  
Db 61 GAGTGTGATTCGTGCTGCTTTTCTGACGAGGCTGCACTGCGGAGTCTGCTGAGAGC 120  
Qy 138 GAGTGTGATTCGTGCTGCTTTTCTGACGAGGCTGCACTGCGGAGTCTGCTGAGAGC 138  
Db 138 GAGTGTGATTCGTGCTGCTTTTCTGACGAGGCTGCACTGCGGAGTCTGCTGAGAGC 138

121 CAACGAGAAATACGCGGAGATCTGTCTCTGCCCCCTAGACTACGAGACCCCTGCGGGGCC 180  
139 CAACGAGAAATACGCGGAGATCTGTCTCTGCCCCCTAGACTACGAGACCCCTGCGGGGCC 198  
181 TACTCTCCGTTACTACTACGACAGGTACAGGACAGGCGCGGAGTTCCGTACGAGG 240  
199 TACTCTCCGTTACTACTACGACAGGTACAGGACAGGCGCGGAGTTCCGTACGAGG 258  
241 GCTGCGAGGCGCAACGCAATTTCTACCTGTGAGGCTTTCAGACGATGCTTGTGGA 300  
259 GCTGCGAGGCGCAACGCAATTTCTACCTGTGAGGCTTTCAGACGATGCTTGTGGA 318  
301 GGATGAGAAAGTTTCCCAAGTTTCCGCTGCAAGTGAAGTGTGACGACGATGTGAG 360  
319 GGATGAGAAAGTTTCCCAAGTTTCCGCTGCAAGTGAAGTGTGACGACGATGTGAG 378  
361 GGTCCACAGAAAGATTTCTTATCTTAAGTTCATGACATGACATGACATGACATGAC 420  
379 GGTCCACAGAAAGATTTCTTATCTTAAGTTCATGACATGACATGACATGACATGAC 438  
421 GTGGGTGTACCGGAGACCGGATTTGAGAACAGGTTTCCAGATGAACTACTTGTATGAG 480  
439 GTGGGTGTACCGGAGACCGGATTTGAGAACAGGTTTCCAGATGAACTACTTGTATGAG 498  
481 TCTGCGCACCAAGAAATTTCCATCATTTTGTCTACAGTCCAAAGATGAGGAGCTGTCT 540  
499 TCTGCGCACCAAGAAATTTCCATCATTTTGTCTACAGTCCAAAGATGAGGAGCTGTCT 558  
541 CTGCGCAATGTGACGTGCTTATTTTATCCAGATGACAGAACTGTATGCTTCACT 600  
559 CTGCGCAATGTGACGTGCTTATTTTATCCAGATGACAGAACTGTATGCTTCACT 618  
601 ATACTGCTGTGAGGAGGATGACATTAATTTGTAGAGGAGGATTTGCAAACTGTGAT 660  
619 ATACTGCTGTGAGGAGGATGACATTAATTTGTAGAGGAGGATTTGCAAACTGTGAT 678  
661 GTGCAAAAGCTTTGAAAGAAAGAAAGATGCCAAAGCTTGTGCTTCCAGTAGAATCC 720  
679 GTGCAAAAGCTTTGAAAGAAAGAAAGATGCCAAAGCTTGTGCTTCCAGTAGAATCC 738  
721 GGAAGAAATTCGGAAGAGCAATTTTAAACATTTCTTAATATGACATGCTTGTCTTAA 780  
739 GGAAGAAATTCGGAAGAGCAATTTTAAACATTTCTTAATATGACATGCTTGTCTTAA 798  
781 GCTTATTTGCTTATGTTGTATCTGAAGATTAATGACAGATGAGAAACAATCA 840  
799 GCTTATTTGCTTATGTTGTATCTGAAGATTAATGACAGATGAGAAACAATCA 858  
841 TTGCGATTTTATTCACAGTTTATTAATACAGTCACTTTTCAAAAATTTGGATTTT 900  
859 TTGCGATTTTATTCACAGTTTATTAATACAGTCACTTTTCAAAAATTTGGATTTT 918  
901 TTTAATATTAATCTACTGCTATCAAAATGTGAGTACACATTTTAAATTTATGTTTAC 960  
919 TTTAATATTAATCTACTGCTATCAAAATGTGAGTACACATTTTAAATTTATGTTTAC 978  
961 TGTGTGAGACTGAATTC 979  
979 TGTGTGAGACTGAATTC 997

RESULT 7  
US-09-949-016-864  
; Sequence 864, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CLO01037  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14

;; PRIOR APPLICATION NUMBER: 60/241,755  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/237,768  
;; PRIOR FILING DATE: 2000-10-03  
;; PRIOR APPLICATION NUMBER: 60/231,498  
;; PRIOR FILING DATE: 2000-09-08  
;; NUMBER OF SEQ ID NOS: 207012  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 864  
;; LENGTH: 1142  
;; TYPE: DNA  
;; ORGANISM: Human  
US-09-949-016-864  
Query Match 99.3%; Score 972.2; DB 3; Length 1142;  
Best Local Similarity 99.7%; Pred. No. 1.6e-262;  
Matches 974; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
1 GGAAGCTTTGCCAGGCGGCGCGCCGACCCCTGACACATGAGACCCGCTGCCCCCTG 60  
19 GGAAGCTTTGCCAGGCGGCGCGCCGACCCCTGACACATGAGACCCGCTGCCCCCTG 78  
61 GGCTGTGATTTCTGCTTTTCTTGAAGAGCTGAGCTGAGGAGATGCTCTGAGAGC 120  
79 GGCTGTGATTTCTGCTTTTCTTGAAGAGCTGAGCTGAGGAGATGCTCTGAGAGC 138  
121 CAACGAGAAATACGCGGAGATCTGTCTCTGCCCCCTAGACTACGAGACCCCTGCGGGGCC 180  
139 CAACGAGAAATACGCGGAGATCTGTCTCTGCCCCCTAGACTACGAGACCCCTGCGGGGCC 198  
181 TACTCTCCGTTACTACTACGACAGGTACAGGACAGGCGCGGAGTTCCGTACGAGG 240  
199 TACTCTCCGTTACTACTACGACAGGTACAGGACAGGCGCGGAGTTCCGTACGAGG 258  
241 GCTGCGAGGCGCAACGCAATTTCTACCTGTGAGGCTTTCAGACGATGCTTGTGGA 300  
259 GCTGCGAGGCGCAACGCAATTTCTACCTGTGAGGCTTTCAGACGATGCTTGTGGA 318  
301 GGATGAGAAAGTTTCCCAAGTTTCCGCTGCAAGTGAAGTGTGACGACGATGTGAG 360  
319 GGATGAGAAAGTTTCCCAAGTTTCCGCTGCAAGTGAAGTGTGACGACGATGTGAG 378  
361 GGTCCACAGAAAGATTTCTTATCTTAAGTTCATGACATGACATGACATGACATGAC 420  
379 GGTCCACAGAAAGATTTCTTATCTTAAGTTCATGACATGACATGACATGACATGAC 438  
421 GTGGGTGTACCGGAGACCGGATTTGAGAACAGGTTTCCAGATGAACTACTTGTATGAG 480  
439 GTGGGTGTACCGGAGACCGGATTTGAGAACAGGTTTCCAGATGAACTACTTGTATGAG 498  
481 TCTGCGCACCAAGAAATTTCCATCATTTTGTCTACAGTCCAAAGATGAGGAGCTGTCT 540  
499 TCTGCGCACCAAGAAATTTCCATCATTTTGTCTACAGTCCAAAGATGAGGAGCTGTCT 558  
541 CTGCGCAATGTGACGTGCTTATTTTATCCAGATGACAGAACTGTGATGCTTCACT 600  
559 CTGCGCAATGTGACGTGCTTATTTTATCCAGATGACAGAACTGTGATGCTTCACT 618  
601 ATACTGCTGTGAGGAGGATGACATTAATTTGTAGAGGAGGATTTGCAAACTGTGAT 660  
619 ATACTGCTGTGAGGAGGATGACATTAATTTGTAGAGGAGGATTTGCAAACTGTGAT 678  
661 GTGCAAAAGCTTTGAAAGAAAGAAAGATGCCAAAGCTTGTGCTTCCAGTAGAATCC 720  
679 GTGCAAAAGCTTTGAAAGAAAGAAAGATGCCAAAGCTTGTGCTTCCAGTAGAATCC 738  
721 GGAAGAAATTCGGAAGAGCAATTTTAAACATTTCTTAATATGACATGCTTGTCTTAA 780  
739 GGAAGAAATTCGGAAGAGCAATTTTAAACATTTCTTAATATGACATGCTTGTCTTAA 798  
781 GCTTATTTGCTTATGTTGTATCTGAAGATTAATGACAGATGAGAAACAATCA 840  
799 GCTTATTTGCTTATGTTGTATCTGAAGATTAATGACAGATGAGAAACAATCA 858

QY	841	TTGGGATTTATTCACCGCTTTTATATACAGCACCTTTCAAAATTTGAGTTT	900
Db	859	TTGGGATTTATTCACCGCTTTTATATACAGCACCTTTCAAAATTTGAGTTT	918
QY	901	TTTATATATTAAGTCTGCTATTCAAATGAGTCTACCACTTTTATATGTTCAAC	960
Db	919	TTTATATATTAAGTCTGCTATTCAAATGAGTCTACCACTTTTATATGTTCAAC	978
QY	961	TGTTTGAGACTGAAT	977
Db	979	TGTTTGAGACTGAAT	995

RESULT 8  
US-08-817-145-2  
; Sequence 2, Application US/08817145  
; Patent No. 6025329  
; GENERAL INFORMATION:

Methods treat  
ophthalmic disease

Oy	121	TAACAGGAAATTAAGCGGAGATCTGTCTCGGCCCTTGACTACAGAACCTCTCGGGGCC	180
Db	131	CAACAGGAAATTAAGCGGAGATCTGTCTCGGCCCTTGACTACAGAACCTCTCGGGGCC	190
Oy	181	TACTTCTCCGTACTACTACGACAGGTACACGACAGAGCTCGCCAGTCTCTACGAGG	240
Db	191	TACTTCTCCGTACTACTACGACAGGTACACGACAGAGCTCGCCAGTCTCTACGAGG	250
Oy	241	GCTGCGAGGCGAACGCGCAAAATTTCTACACTGCGAGGCTTGGCGACGATGCTGTGGA	300
Db	251	GCTGCGAGGCGAACGCGCAAAATTTCTACACTGCGAGGCTTGGCGACGATGCTGTGGA	310
Oy	301	GGATTAAGAAAAAGTTCCCAAGGTTGCCGCGTACGATGCTGGACGACGACGATGAGG	360
Db	311	GGATTAAGAAAAAGTTCCCAAGGTTGCCGCGTACGATGCTGGACGACGACGATGAGG	370
Oy	361	GGTCCACAGAAAAAGTATTTCTTTAATCTAAGTTCATGACATGTGAAAAATTTCTTTCCG	420
Db	371	GGTCCACAGAAAAAGTATTTCTTTAATCTAAGTTCATGACATGTGAAAAATTTCTTTCCG	430
Oy	421	GTGGGTGTCAACCGGAACCGGATTTGAGAACGGTTTCCAGATGACGTACTTGTATGGGCT	480
Db	431	GTGGGTGTCAACCGGAACCGGATTTGAGAACGGTTTCCAGATGACGTACTTGTATGGGCT	490
Oy	481	TCTGCGCACCAAAAGAAATTCATATTTTGCTACAGTCCAAAAGATGAGGACCTGTGCT	540
Db	491	TCTGCGCACCAAAAGAAATTCATATTTTGCTACAGTCCAAAAGATGAGGACCTGTGCT	550
Oy	541	CTGCGCAATGTAAGTCTGCTAATTAATTTAATTCAGAGTACAGAACCTGTGATGCTTCACT	600
Db	551	CTGCGCAATGTAAGTCTGCTAATTAATTTAATTCAGAGTACAGAACCTGTGATGCTTCACT	610
Oy	601	ATACTGCGTGTGAGGAGATGACATTAATCTTTGTAGCAGGAGATTCGCAACGTGCAT	660
Db	611	ATACTGCGTGTGAGGAGATGACATTAATCTTTGTAGCAGGAGATTCGCAACGTGCAT	670
Oy	661	GTGCAAAAGCTTTGAAAAAGAAAAAGAAAGATCCCAAAGCTTGCTTGCCAGTGAATCC	720
Db	671	GTGCAAAAGCTTTGAAAAAGAAAAAGAAAGATCCCAAAGCTTGCTTGCCAGTGAATCC	730
Oy	721	GGAAAAATCCGAAAGAAATTTTAAACATCTCTTAATATGTCATCTGTGTGCTTATG	780
Db	731	GGAAAAATCCGAAAGAAATTTTAAACATCTCTTAATATGTCATCTGTGTGCTTATG	790
Oy	781	GCTTATTTGCTTTATGTTGTGTATCTGAAGATTAATATGACAGATGAGAAACAATCA	840
Db	791	GCTTATTTGCTTTATGTTGTGTATCTGAAGATTAATATGACAGATGAGAAACAATCA	850
Oy	841	TTGGTGATTTATCCAGATTTTATTAATACAAAGTCACTTTTCAAAAAATTTGAATTT	900
Db	851	TTGGTGATTTATCCAGATTTTATTAATACAAAGTCACTTTTCAAAAAATTTGAATTT	910
Oy	901	TTTATATATTAATAGCTGTATTTCAAATGTAGTGTACACATTTTAAATTTAAGTCAAC	960
Db	911	TTTATATATTAATAGCTGTATTTCAAATGTAGTGTACACATTTTAAATTTAAGTCAAC	970
Oy	961	TGTTTGTAGACTGAATTC	979
Db	971	TGTTTGTAGACTGAATTC	989

RESULT 9  
US-09-702-705-64  
Sequence 64, Application US/09702705  
Parent No. 6504010  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Lodges, Michael A.  
APPLICANT: Fanger, Gary  
APPLICANT: Vedvick, Tom  
APPLICANT: Carrier, Derrick  
APPLICANT: Retter, Marc

```
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 64
LENGTH: 528
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(528)
OTHER INFORMATION: n = A,T,C or G
US-09-702-705-64
```

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Query Match 45.7%; Score 447; DB 3; Length 528;
Best Local Similarity 87.5%; Pred.No. 2.7e-115;
Matches 440; Conservative 42; Mismatches 20; Indels 1; Gaps 1;
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```
QY 1 GGAGCGCTTGGCCAGCGGGCGGCCGACCCCTGACCATGAGACCCCGTGGCCCTGG 60
DB 27 SGAGCGCTTGGCCAGCGGGCGGCCGACCCCTGSRCCATGAGACCCCGTGGCCCTGG 86
QY 61 GGCTGTGATTCGTGCTTTTCTGACGAGAGCTGCACTGGCGATGCTGCTCAGAGC 120
DB 87 GGMTTGTATCTGCTGCTTTTCTGRCGAGAGCTGCACTGGCGATGCTATCARAGC 146
QY 121 CAACGAGAAATPACGCGAGATCTGCTCTGCCCCCTAGACTAGAGACCTGCGCGGCC 180
DB 147 CAACGAGAAATPACRCGAGATCTGCTCTGCCCCCTAGACTAGAGACCTGCGCGGCC 206
QY 181 TACTTCTCGTTACTACTACGAGATGACGAGAGCTGCGCGAGTTCCTGTACGGGG 240
DB 207 TACTTTCGGTACTACTACGAGATGACGAGAGCTGCGCGAGTTCCTGTACGGGG 266
QY 241 GCTGCGAGGGCAACGCCCAATTTCTACACTGGAGGCTTGCAGATGCTTCTGGA 300
DB 267 GCTGCRABGGCAACGCCCAATTTCTACACCKGAGGATTCACATGCTGCTWSTGGA 326
QY 301 GGATGAGAAAAGTTCCCAAGTTTCCCGCTGCAAGTAGAGTGAGCAACAAGTGAGG 360
DB 327 RGATGAGAAAAGTTCCCAAGTTTCCCGCTGMAAGTAGAGTAGAGCAACAAGGAGG 386
QY 361 GGTCCACGAGAAAGTATTTCTTAATCTAAGTTCCATGACATGAGAAAATTTCTTTCG 420
DB 387 GGTACACAGATTAAGTATTTCTTAATCTAARKWCATGACATGAGAAAATTTCTTNNCG 446
QY 421 GTGGGTGTCAACCGAACCAGATTGAGAACAGGTTTCCAGATGAAGCTACTGTATGGCT 480
DB 447 GTGGNGTCAACCGG-ACCGAGTTGAGAACANGTTTTCAGATGANGCTACTGGATGGCT 505
QY 481 TCTGCGCACCAAGAAAATTCCA 503
DB 506 CCTGCRCAACNAAGAAANTATCA 528
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RESULT 10
US-09-736-457-64
Sequence 64, Application US/09736457
Patent No. 6509448
GENERAL INFORMATION:
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APPLICANT: Wang, Tonglong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
```

```
APPLICANT: Fan, Liqun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 64
LENGTH: 528
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(528)
OTHER INFORMATION: n = A,T,C or G
US-09-736-457-64
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Query Match 45.7%; Score 447; DB 3; Length 528;
Best Local Similarity 87.5%; Pred.No. 2.7e-115;
Matches 440; Conservative 42; Mismatches 20; Indels 1; Gaps 1;
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QY 1 GGAGCGCTTGGCCAGCGGGCGGCCGACCCCTGACCATGAGACCCCGTGGCCCTGG 60
DB 27 SGAGCGCTTGGCCAGCGGGCGGCCGACCCCTGSRCCATGAGACCCCGTGGCCCTGG 86
QY 61 GGCTGTGATTCGTGCTTTTCTGACGAGAGCTGCACTGGCGATGCTGCTCAGAGC 120
DB 87 GGMTTGTATCTGCTGCTTTTCTGRCGAGAGCTGCACTGGCGATGCTATCARAGC 146
QY 121 CAACGAGAAATPACGCGAGATCTGCTCTGCCCCCTAGACTAGAGACCTGCGCGGCC 180
DB 147 CAACGAGAAATPACRCGAGATCTGCTCTGCCCCCTAGACTAGAGACCTGCGCGGCC 206
QY 181 TACTTCTCGTTACTACTACGAGATGACGAGAGCTGCGCGAGTTCCTGTACGGGG 240
DB 207 TACTTTCGGTACTACTACGAGATGACGAGAGCTGCGCGAGTTCCTGTACGGGG 266
QY 241 GCTGCGAGGGCAACGCCCAATTTCTACACTGGAGGCTTGCAGATGCTTCTGGA 300
DB 267 GCTGCRABGGCAACGCCCAATTTCTACACCKGAGGATTCACATGCTGCTWSTGGA 326
QY 301 GGATGAGAAAAGTTCCCAAGTTTCCCGCTGCAAGTAGAGTGAGCAACAAGTGAGG 360
DB 327 RGATGAGAAAAGTTCCCAAGTTTCCCGCTGMAAGTAGAGTAGAGCAACAAGGAGG 386
QY 361 GGTCCACGAGAAAGTATTTCTTAATCTAAGTTCCATGACATGAGAAAATTTCTTTCG 420
DB 387 GGTACACAGATTAAGTATTTCTTAATCTAARKWCATGACATGAGAAAATTTCTTNNCG 446
QY 421 GTGGGTGTCAACCGAACCAGATTGAGAACAGGTTTCCAGATGAAGCTACTGTATGGCT 480
DB 447 GTGGNGTCAACCGG-ACCGAGTTGAGAACANGTTTTCAGATGANGCTACTGGATGGCT 505
QY 481 TCTGCGCACCAAGAAAATTCCA 503
DB 506 CCTGCRCAACNAAGAAANTATCA 528
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RESULT 11
US-09-614-124B-64
Sequence 64, Application US/09614124B
Patent No. 6630574
GENERAL INFORMATION:
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APPLICANT: Wang, Tonglong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
```

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1 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
2 TITLE OR INVENTION: DIAGNOSIS OF LUNG CANCER
3 FILE REFERENCE: 210121.478C3
4 CURRENT APPLICATION NUMBER: US/09/614,124B
5 CURRENT FILING DATE: 2001-07-11
6 NUMBER OF SEQ ID NOS: 1668
7 SOFTWARE: FastSeq for Windows Version 3.0
8 SEQ ID NO 64
9 LENGTH: 528
10 TYPE: DNA
11 ORGANISM: Homo sapien
12 FEATURE:
13 NAME/KEY: mlec_feature
14 LOCATION: (1)...(528)
15 OTHER INFORMATION: n = A,T,C or G
16 US-09-614-124B-64

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Query Match	45.7%	Score 447;	DB 3;	Length 528;
Best Local Similarity	87.5%	Pred. No. 2.7e-115;		
Matches 440;	Conservative 42;	Mismatches 20;	Indels 1;	Gaps 1

[illegible]

RESULT 12  
 US-09-671-325-64  
 Sequence 64, Application US/09671325  
 Patent No. 6667154  
 GENERAL INFORMATION:  
 APPLICANT: Wang, Tongtong  
 APPLICANT: Bangur, Chaitanya S.  
 APPLICANT: Lodes, Michael A.  
 APPLICANT: Fanger, Gary  
 APPLICANT: Vedvick, Tom  
 APPLICANT: Carter, Darrick  
 APPLICANT: Retter, Marc  
 APPLICANT: Mannion, Jane  
 APPLICANT: Pan, Liqun  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

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? TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
? FILE REFERENCE: 210121.476C12
? CURRENT APPLICATION NUMBER: US/09/671,325
? CURRENT FILING DATE: 2000-09-26
? NUMBER OF SEQ ID NOS: 1825
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO: 64
? LENGTH: 528
? TYPE: DNA
? ORGANISM: Homo sapien
? FEATURES:
? NAME/KEY: misc feature
? LOCATION: (1)...(528)
? OTHER INFORMATION: n = A,T,C or G
US-09-671-325-64

```

Query Match	45.7%	Score 447;	DB 3;	Length 528;
Best Local Similarity	87.5%;	Pred. No. 2.7e-115;		
Matches 440;	Conservative 42;	Mismatches 20;	Indels 1;	Gaps 1;

[illegible]

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RESULT 13
US-09-589-184-64
; Sequence 64, Application US/09589184
; Patent No. 6686447
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongrong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C8

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Query Match	45.7%;	Score 447;	DB 3;	Length 528;
Best Local Similarity	87.5%;	Pred. No. 2.7e-115;		
Matches 440;	Conservative 42;	Mismatches 20;	Indels 1;	Gaps 1

Qy	1	GGAGGCGCTTGCCCAAGGAGGGGCGCCCGAACCCCTGACCATGGAACCCCGCTGAGCCCGTGG	60
Db	27	SGACGCGCTTGCCCAAGGAGGGGCGCCCGAACCCCTGSRCAATGGAACCCCGCTGAGCCCGTGG	86
Qy	61	GGCTGTGCAATGTGCTGTGCTTTTCTGACGGAAGCTGCACTGGGCGATGTGCTCAGAGAC	120
Db	87	GGATGTGTGATKCTGCTGCTTTTCTGTGRCGAGGCTGCACTGGGCGATGTGCTATCARGAGC	146
Qy	121	CAACAGAGAAATTAACGCGAGAGATCTGTGCTCTGCGCCCTTGACTACAGAACCTGCGCGAGCC	180
Db	147	CAACAGAGAAATTAACGCGAGAGATCTGTGCTCTGCGCCCTTGACTACAGAACCTGCGCGAGCC	206
Qy	181	TACTTCTCCGTTACTACTACGACAGGTACGCGAGAGCTGCGCGCAATTCCTGTACGAGG	240
Db	207	TACTTCTCCGTTACTACTACGACAGGTACGCGAGAGCTGCGCGCAATTCCTGTGRCAGG	266
Qy	241	GCTGCGAGGGCAACGCGCAACAATTTCTACCTGGGAGGCTTGGAGAGATGCTTGCTGAG	300
Db	267	GCTGCGAAGGCAACGCGCAACAATTTCTACCTGGGAGGCTTGGAGAGATGCTTGCTGAG	326
Qy	301	GGATAGAAAAAGTTCCCAAGTTTGCGGGCTGCAAGTAGTGTGAGCGACCAAGTGTAGG	366
Db	327	GGATAGAAAAAGTTCCCAAGTTTGCGGGCTGMAAGTAGAGCAACCAAGGTGTAGG	386
Qy	361	GGTCCACAAAAAGTATTTCTTAATCTTAAGTTCATGATGCAATGAGAAAAATTTCTTTCCG	420
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Qy	421	GTGGGTGTCAACCGGAACCGGATTGAGAACAGGTTTCCAGATGAAGCTACTGTATGGCT	480
Db	447	GTGGGTGTCAACCGG-AACGGATTGAGAACAGTTTTCAGATGAGCTACTGGATGGCT	505
Qy	481	TTCTGCGCAACCAAGAAAAATTCCA	503
Db	506	CTGTGRCACAAAAAANAATATCA	528

RESULT 14 US-09-658-824-64  
 / Sequence 64, Application US/09568824  
 / Patent No. 6746846  
 / GENERAL INFORMATION:  
 / APPLICANT: Wang, Tongtong  
 / APPLICANT: Bangur, Chaitanya S.  
 / APPLICANT: Lodes, Michael A.  
 / APPLICANT: Fanger, Gary  
 / APPLICANT: Vedwick, Tom  
 / APPLICANT: Carter, Darlick  
 / APPLICANT: Retter, Marc  
 / APPLICANT: Mannion, Jane  
 / APPLICANT: Fan, Liqun  
 / TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
 / TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER  
 / FILE REFERENCE: 210121.478C11  
 / CURRENT APPLICATION NUMBER: US/09/658, 824

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? CURRENT FILING DATE: 2000-09-08
? NUMBER OF SEQ ID NOS: 1788
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 64
? LENGTH: 528
? TYPE: DNA
? ORGANISM: Homo sapien
? FEATURES:
? NAME/KEY: misc feature
? LOCATION: (1)..(528)
? OTHER INFORMATION: n = A,T,C OR G
US-03-658-824-64

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Query Match	45.7%	Score 447	DB 3	Length 528
Best Local Similarity	87.5%	Pred. No. 2.7e-115		
Matches 440	Conservative 42	Mismatches 20	Indels 1	Gaps 1

Qy	1	GGAGGCGCTTGCCGAGGGGCGCGCGGACCCCTGACACATGAGACCCCGCTGCGCCCTGG	60
Db	27	SGAGCGCTTGCCGAGGGGCGCGCGGACCCCTGSRCAATGAGACCCCGCTGCGCCCTGG	86
Qy	61	GGCTGCGATTCGTGCTGCTTTTCTTGACGAGAGGCTGCACTGAGGCGATGCTGTCAGAGNC	120
Db	87	GGATGTGTATKCTGCTGCTTTTCTTGSRCKAGAGCTGCACTGAGCGATGCTGATCARAGC	146
Qy	121	CAACAGAAATTAACGAGAGATCTGTCTCTGAGCCCTTGACTGACGAGACCCGCGCGGCCC	180
Db	147	CAACAGAAATTAACGAGAGATCTGTCTCTGAGCCCTTGACTGACGAGACCCGCGCGGCCC	206
Qy	181	TACTCTCCGTTACTACTACGACAGGTACACGACAGGCTGCGCGAGTTCTCTGTAACGGG	240
Db	207	TACTTCTCGGTACTACTACGACAGGTACACGACAGGCTGCGCGAGTTCTCTGTRCKGGG	266
Qy	241	GCTGCGAGGGGCAACGCGCAATTTCTACCTGGGAGGCTTGCGAGATGCTTGCTGAGCA	300
Db	267	GCTGCGAASGCAACGCGCAATTTCTACCTGGGAGGCTTGCGAGATGCTTGCTGAGCA	326
Qy	301	GGATGAAAAAGTTCCCAAGTTTGC CGGCTGCAAGTAGTGTGAGCAACCAAGTGTAGG	366
Db	327	GGATGAAAAAGTTCCCAAGTTTGC CGGCTGMAAGTAGAAGAGCAACCAAGGTTAGG	386
Qy	361	GGTCCACAAAAAGATTTCTTTATCTTAATTCATATTCATGACATGAGAAAAATTCCTTTCCG	420
Db	387	GGTACCAATTAAGATTTCTTTATCTTAATTCATATTCATGACATGAGAAAAATTCCTTTNCG	446
Qy	421	GTGGGTTGCAACCGGAAACCGATTGAGAACAGGTTTCCAGATGAGACTTGTATGAGCT	480
Db	447	GTGGGTTGCAACCGGAAACCGATTGAGAACAGGTTTCCAGATGAGACTTGTATGAGCT	505
Qy	481	TCGTGCGACCAAGAAATTCACA 503	
Db	506	CTGTGCGACCAAGAAATTCACA 528	

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RESULT 15
US-10-017-754-64
: Sequence 64, Application US/10017754
: Patent No. 6858204
: GENERAL INFORMATION:
: APPLICANT: Henderson, Robert A.
: APPLICANT: Wang, Tongtong
: APPLICANT: Matsubae, Yoshihiro
: APPLICANT: Johnson, Jeffrey C.
: APPLICANT: Retter, Marc W.
: APPLICANT: Marnierakis, Margarita
: APPLICANT: Carter, Darrick
: APPLICANT: Fanger, Gary R.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: McNabb, Andrea
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.478C18

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/ CURRENT APPLICATION NUMBER: US/10/017,754
/ CURRENT FILING DATE: 2001-10-29
/ NUMBER OF SEQ ID NOS: 2004
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 64
/ LENGTH: 528
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 374, 443, 444, 452, 476, 489, 515, 523
/ OTHER INFORMATION: n = A,T,C or G
US-10-017-754-64
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Query Match 45.7%; Score 447; DB 3; Length 528;
Best Local Similarity 87.5%; Pred.No. 2.7e-115;
Matches 440; Conservative 42; Mismatches 20; Indels 1; Gaps 1;
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OY 1 GGAAGCCCTTGCCAGAGGAGCGCGCCGACCCCTGACACATGAGACCCCGCTGCGCCCTGG 60
DB 27 SGACCCCTTGCCAGAGGAGCGCGCCGACCCCTGSRCAATGACCCCGCTGCGCCCTGG 86
OY 61 GAGCTGCAATTCGTGCTTTTCTGACGAGAGCTGCACTGGCGATGCTGCTCAGAGC 120
DB 87 GAGTGTGATKCTGCTGCTTTTCTGRCAGAGGCTGCACTGGCGATGCTGATCARAGC 146
OY 121 CAACGGAATTAACGGGAGATCTGCTCTGCGCCCTAGACTACGACCTGCGCGGCC 180
DB 147 CAACGGAATTAACGAGATCTGCTCTGCGCCCTAGACTACGACCTGCGCGGCC 206
OY 181 TACTTCTCGGTACTACTACGACAGGTACAGGAGCTGCGCGAGTTCTGTACGAGG 240
DB 207 TACTTCTCGGTACTACTACGAGGTACAGGAGCTGCGCGAGTTCTGTACGAGG 266
OY 241 GCTGCGAGGCAACGCCCAATTTCTACCTGAGAGGCTTGCAAGATGCTTGCTGA 300
DB 267 GCTGCGAGGCAACGCCCAATTTCTACCTGAGAGGCTTGCAAGATGCTTGCTGA 326
OY 301 GGATGAAAAAGTTCCCAAGTTTGCAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 360
DB 327 GGATGAAAAAGTTCCCAAGTTTGCAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 386
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DB 387 GGTACACAGATTAAGTATTTCTTAATCTAAGTTCAATGACATGTAATAAATCTTTNCG 446
OY 421 GTGGGTGTCAACCGAACCGATTTGAGAACAGGTTTCAAGATGAAGCTACTTATGGGCT 480
DB 447 GTGGGTGTCAACCGG-AACGGAATTGAGAACAGGTTTCAAGATGAAGCTACTTATGGGCT 505
OY 481 TCTGCGCAACCAAAAGAAATTTCA 503
DB 506 CTTGCRACANAAAGAAATATATCA 528
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Search completed: March 11, 2006, 06:08:17  
Job time : 226 secs

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Db      161 TACTTCTCCGTTAAGTAACTGACAGAGTACAGCAAGCTGCGCAAGTCTGTACGGAG 240
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Db      301 GGATGAAAAAGTTGCCAAAGTTTCCGGCTCAAGTGAAGTGTGACGACGAGTGTGAG 360
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Qy      481 TGTGGGCAACCAAAAGAAATTCATCATTTTGTCTACAGTCCAAAGATGAGGAGCTGTCT 540
Db      481 TGTGGGCAACCAAAAGAAATTCATCATTTTGTCTACAGTCCAAAGATGAGGAGCTGTCT 540
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Qy      661 GTGCAAAAAGCTTTGAAAAAGAAAGAGATGCCAAAGCTTGGCTTGGCAATGATCC 720
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Db      781 GCTTATTTGCTTTATGTTGTTATCTGAAATGAAATATATGACAGATGAGAAACAAATCA 840
Qy      841 TTGGGATTTATTTACACAGATTTTATTAATCAAGTCACTTTTCAAAAATTTGATTTT 900
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Qy      901 TTTATATATTAATCTAGCTGCTATTTCAAAATGTGATCTACCATTTTAAATTTATGTTCAAC 960
Db      901 TTTATATATTAATCTAGCTGCTATTTCAAAATGTGATCTACCATTTTAAATTTATGTTCAAC 960
Qy      961 TGTGTGTGAGACTGAATTC 979
Db      961 TGTGTGTGAGACTGAATTC 979

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RESULT 2  
US-10-305-720-1378

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; Sequence 1378, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1378
; LENGTH: 979
; TYPE: DNA

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Genbank ID No. US20040010136A1 9441149
US-10-305-720-1378

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Query Match 100.0%; Score 979, DB 6; Length 979;  
Best Local Similarity 100.0%; Pred. No. 2,8e-247;  
Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      121 CAACGAGAAATTAAGCGGAGATCTGTCTCTGCCCCCTTGACTAGGAACTTGCAGGCCC 180
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Qy      421 GTGGGTGTCAACCGGAAACCGGATTTGAGAACAGGTTTCCAGATGACCTATTGTATG 480
Db      421 GTGGGTGTCAACCGGAAACCGGATTTGAGAACAGGTTTCCAGATGACCTATTGTATG 480
Qy      481 TGTGGGCAACCAAAAGAAATTCATCATTTTGTCTACAGTCCAAAGATGAGGAGCTGTCT 540
Db      481 TGTGGGCAACCAAAAGAAATTCATCATTTTGTCTACAGTCCAAAGATGAGGAGCTGTCT 540
Qy      541 CTGGCAATGTGACTGCTATTTATTTTAATCCAGATGACAGACCTGTATGCTTCACT 600
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Qy      601 ATACTGCTGTGAGGAGATGACAAATTAATTGTTAGCAGGAGATTTGCAACCTGTGAT 660
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Qy      661 GTGCAAAAAGCTTTGAAAAAGAAAGATGCCAAAGCTTGGCTTGGCAATGATCC 720
Db      661 GTGCAAAAAGCTTTGAAAAAGAAAGATGCCAAAGCTTGGCTTGGCAATGATCC 720
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Db      721 GAAAAATTCGAAAGAGCAATTTTAAACATTTCTTAATGTGCAATCTTGTGTCTTTA 780
Qy      781 GCTTATTTGCTTTATGTTGTTATCTGAAATGAAATATATGACAGATGAGAAACAAATCA 840
Db      781 GCTTATTTGCTTTATGTTGTTATCTGAAATGAAATATATGACAGATGAGAAACAAATCA 840
Qy      841 TTGGGATTTATTTACACAGATTTTATTAATCAAGTCACTTTTCAAAAATTTGATTTT 900
Db      841 TTGGGATTTATTTACACAGATTTTATTAATCAAGTCACTTTTCAAAAATTTGATTTT 900
Qy      901 TTTATATATTAATCTAGCTGCTATTTCAAAATGTGATCTACCATTTTAAATTTATGTTCAAC 960
Db      901 TTTATATATTAATCTAGCTGCTATTTCAAAATGTGATCTACCATTTTAAATTTATGTTCAAC 960

```

Oy 961 TGTGTGAGACTGAATTC 979  
Db 961 TGTGTGAGACTGAATTC 979

## RESULT 3

US-10-680-684-1

Sequence 1, Application US/10680684  
Publication No. US20040253686A1  
GENERAL INFORMATION:  
APPLICANT: Sprechel, Cindy A.  
APPLICANT: Kiesel, Walter  
APPLICANT: Foster, Donald C.  
TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS  
TITLE OF INVENTION: AND  
FILE REFERENCE: 93-14D3  
CURRENT APPLICATION NUMBER: US/10/680,684  
CURRENT FILING DATE: 2003-10-07  
PRIOR APPLICATION NUMBER: US/09/904,621  
PRIOR FILING DATE: 2001-07-13  
PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: 09/265,627  
PRIOR FILING DATE: PRIOR FILING DATE: 1999-03-09  
PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: 5,455,338  
PRIOR FILING DATE: PRIOR FILING DATE: 1993-11-05  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 979  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (39) ... (746)  
US-10-680-684-1

Query Match 100.0%; Score 979; DB 8; Length 979;

Best Local Similarity 100.0%; Pred. No. 2.8e-247; Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GAAGCGCTTGGCCAGCGGGCGCGCCCGCTGACCATGAGACCCCGCTGCGCCCTGCG 60  
Db 1 GAAGCGCTTGGCCAGCGGGCGCGCCCGCTGACCATGAGACCCCGCTGCGCCCTGCG 60  
Oy 61 GCGTGTGATTCGTGCTGCTTTTCTGACGAGGCTGCACTGCGCGATGCTGCTCAGAGC 120  
Db 61 GCGTGTGATTCGTGCTGCTTTTCTGACGAGGCTGCACTGCGCGATGCTGCTCAGAGC 120  
Oy 121 CAACAGGAAATTAACCGGAGATCTGCTCTCCCTGACATGAGACCCCTGCGGGGCC 180  
Db 121 CAACAGGAAATTAACCGGAGATCTGCTCTCCCTGACATGAGACCCCTGCGGGGCC 180  
Oy 181 TACTTCTCCGTTACTACTACGACAGGTACAGCAGAGCTGCGCGATGCTGCTGAGGG 240  
Db 181 TACTTCTCCGTTACTACTACGACAGGTACAGCAGAGCTGCGCGATGCTGCTGAGGG 240  
Oy 241 GCTGCGAGGAGCAACGCAATTTCTACCTGAGAGCTTGCAGCAGATGCTGCTGGA 300  
Db 241 GCTGCGAGGAGCAACGCAATTTCTACCTGAGAGCTTGCAGCAGATGCTGCTGGA 300  
Oy 301 GGAATGAAAAGTTCCCAAGTTTCCGGCTGCAAGTGAAGTGAACAAGTGTAGG 360  
Db 301 GGAATGAAAAGTTCCCAAGTTTCCGGCTGCAAGTGAAGTGAACAAGTGTAGG 360  
Oy 361 GGTCCACAGAAAAGTATTTCTTAATCTAAGTTCCATGACATGTGAAAATTTCTTTCCG 420  
Db 361 GGTCCACAGAAAAGTATTTCTTAATCTAAGTTCCATGACATGTGAAAATTTCTTTCCG 420  
Oy 421 GTGGGTGTACCGGAACCGAATTGAGAACAGGTTTCAAGTAAAGCTACTGTATGAGCT 480  
Db 421 GTGGGTGTACCGGAACCGAATTGAGAACAGGTTTCAAGTAAAGCTACTGTATGAGCT 480

Oy 481 TCTGCGACCAAGAAAATTCATCTTTGCTACAGTCCAAAGATGAGGAGCTGCT 540  
Db 481 TCTGCGACCAAGAAAATTCATCTTTGCTACAGTCCAAAGATGAGGAGCTGCT 540  
Oy 541 CTGCGAATGTGACTCGCTATTATTTTAATCCAGATACAGAACTGTGATCTTCACT 600  
Db 541 CTGCGAATGTGACTCGCTATTATTTTAATCCAGATACAGAACTGTGATCTTCACT 600  
Oy 601 ATACTGCTGTGAGGAGAAATGACATTAATCTTTAGAGGAGATTTGCAAGTGCAT 660  
Db 601 ATACTGCTGTGAGGAGAAATGACATTAATCTTTAGAGGAGATTTGCAAGTGCAT 660  
Oy 661 GTGCAAAAAGCTTTGAAAAGAAAAGAGATGCCAAAGCTTGCCTTGCCAGTAGATCC 720  
Db 661 GTGCAAAAAGCTTTGAAAAGAAAAGAGATGCCAAAGCTTGCCTTGCCAGTAGATCC 720  
Oy 721 GGAATAATTCGAGAGCAATTTTAAACATTTTAATATGTCATCTTGTGCTTTATG 780  
Db 721 GGAATAATTCGAGAGCAATTTTAAACATTTTAATATGTCATCTTGTGCTTTATG 780  
Oy 781 GCTTATTTGCTTTATGTTGTATCTGAGAAATATATGACATGAGAGAAACAAATCA 840  
Db 781 GCTTATTTGCTTTATGTTGTATCTGAGAAATATATGACATGAGAGAAACAAATCA 840  
Oy 841 TTGGGATTTATTCACAGTTTATTAATTAACAAGTCACTTTTCAAAAATTTGATTT 900  
Db 841 TTGGGATTTATTCACAGTTTATTAATTAACAAGTCACTTTTCAAAAATTTGATTT 900  
Oy 901 TTTATATTAATCTAGCTGCTAATTCAAATGAGTCTACATTTTAAATTAATGTTCAAC 960  
Db 901 TTTATATTAATCTAGCTGCTAATTCAAATGAGTCTACATTTTAAATTAATGTTCAAC 960  
Oy 961 TGTGTGAGACTGAATTC 979  
Db 961 TGTGTGAGACTGAATTC 979

## RESULT 4

US-10-800-057-1

Sequence 1, Application US/10800057  
Publication No. US2005004021A1  
GENERAL INFORMATION:  
APPLICANT: Sprechel, Cindy A.  
APPLICANT: Kiesel, Walter  
APPLICANT: Foster, Donald C.  
TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS  
TITLE OF INVENTION: AND  
FILE REFERENCE: 93-14D3  
CURRENT APPLICATION NUMBER: US/10/800,057  
CURRENT FILING DATE: 2004-03-12  
PRIOR APPLICATION NUMBER: US/10/680,684  
PRIOR FILING DATE: 2003-10-07  
PRIOR APPLICATION NUMBER: US/09/904,621  
PRIOR FILING DATE: 2001-07-13  
PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: 09/265,627  
PRIOR FILING DATE: PRIOR FILING DATE: 1999-03-09  
PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: 5,455,338  
PRIOR FILING DATE: PRIOR FILING DATE: 1993-11-05  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 979  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (39) ... (746)  
US-10-800-057-1

Query Match 100.0%; Score 979; DB 8; Length 979;  
Best Local Similarity 100.0%; Pred. No. 2.8e-247; Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGCCTTGCCAGAGGCGCCGAGCCCTTGACATGGAACCCCGCTGCCCCCTGG 60  
DB 1 GGAAGCCTTGCCAGAGGCGCCGAGCCCTTGACATGGAACCCCGCTGCCCCCTGG 60  
QY 61 GAGCTGCAATCTGCGCTTTCTGAGGAGGCTGACCTGGGCGATGCTGTCAGAGGC 120  
DB 61 GAGCTGCAATCTGCGCTTTCTGAGGAGGCTGACCTGGGCGATGCTGTCAGAGGC 120  
QY 121 CAACAGAAATACGCGAGATCTGCTCTGCGCCCTAGACTACGACACCTGCGGGCC 180  
DB 121 CAACAGAAATACGCGAGATCTGCTCTGCGCCCTAGACTACGACACCTGCGGGCC 180  
QY 181 TACTTCTCCGTTACTACTACAGAGTACAGCAGAGTCTGCGCACTTCTGTACGG 240  
DB 181 TACTTCTCCGTTACTACTACAGAGTACAGCAGAGTCTGCGCACTTCTGTACGG 240  
QY 241 GCTGGAGAGGCGAAGCGCAATTTCTACACCTGGGAGGCTTGGACGATGCTTGCTGA 300  
DB 241 GCTGGAGAGGCGAAGCGCAATTTCTACACCTGGGAGGCTTGGACGATGCTTGCTGA 300  
QY 301 GGAATGAAAAAGTCCCAAGTTTGCCGCTGCAAGTACGATGAGTGAAG 360  
DB 301 GGAATGAAAAAGTCCCAAGTTTGCCGCTGCAAGTACGATGAGTGAAG 360  
QY 361 GGTCCACAGAAAAATTTCTTTAATCTAAGTTCCATGACATGTAATAATCTTTTCG 420  
DB 361 GGTCCACAGAAAAATTTCTTTAATCTAAGTTCCATGACATGTAATAATCTTTTCG 420  
QY 421 GGGGGTGCACCGGAACCGGATTTGAGAACGGTTTCCAGTAGACTCTGTATAGGGCT 480  
DB 421 GGGGGTGCACCGGAACCGGATTTGAGAACGGTTTCCAGTAGACTCTGTATAGGGCT 480  
QY 481 TCTGCGCACCAAGAAATTTCCATCTTTGCTACAGTCCAAAGATGAGGAGCTGTGCT 540  
DB 481 TCTGCGCACCAAGAAATTTCCATCTTTGCTACAGTCCAAAGATGAGGAGCTGTGCT 540  
QY 541 CTGCGCAATGTGACTGCTATTTATTTTATCCAAAGTACAGAACTGTGATGCTTCACTT 600  
DB 541 CTGCGCAATGTGACTGCTATTTATTTTATCCAAAGTACAGAACTGTGATGCTTCACTT 600  
QY 601 ATACTGGCGTGGAGGAGATGACAACTTTGTTAGCAGGAGGATTTGCAAAAGTGCAT 660  
DB 601 ATACTGGCGTGGAGGAGATGACAACTTTGTTAGCAGGAGGATTTGCAAAAGTGCAT 660  
QY 661 GTGCAAAAGCTTTGAAAAAGAAAGATGCAAGCTTGCCTTGCAGTAGAATCC 720  
DB 661 GTGCAAAAGCTTTGAAAAAGAAAGATGCAAGCTTGCCTTGCAGTAGAATCC 720  
QY 721 GGAATAATCGAAGAGCAATTTTAACTTTAATATGTCATCTTGTGTCTTTATG 780  
DB 721 GGAATAATCGAAGAGCAATTTTAACTTTAATATGTCATCTTGTGTCTTTATG 780  
QY 781 GCTTATTTGCTTTATGTTGTTATCTGAAGATTAATATGACAGTAGAGAAACAAACA 840  
DB 781 GCTTATTTGCTTTATGTTGTTATCTGAAGATTAATATGACAGTAGAGAAACAAACA 840  
QY 841 TTGAGATTTATTCACAGTTTATTTATTAATACAGTCACTTTTCAAAAATTTGATTTT 900  
DB 841 TTGAGATTTATTCACAGTTTATTTATTAATACAGTCACTTTTCAAAAATTTGATTTT 900  
QY 901 TTTATATATTAATAGCTGCTATTTCAATGTGAGTCTACATTTTAAATTTATGTTTCAAC 960  
DB 901 TTTATATATTAATAGCTGCTATTTCAATGTGAGTCTACATTTTAAATTTATGTTTCAAC 960  
QY 961 TGTGTTGAGACTGAATTC 979  
DB 961 TGTGTTGAGACTGAATTC 979

RESULT 5  
US-10-060-036-145  
; Sequence 145, Application US/10060036

; Publication No. US20030073144A1  
; GENERAL INFORMATION:  
; APPLICANT: Benson, Darin R.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Persing, David H.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Jiang, Yugu  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER  
; FILE REFERENCE: 210121.566  
; CURRENT FILING DATE: 2002-01-30  
; NUMBER OF SEQ ID NOS: 4560  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 145  
; LENGTH: 1172  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-060-036-145

Query Match 100.0%; Score 979; DB 5; Length 1172;  
Best Local Similarity 100.0%; Pred. No. 3.1e-247;  
Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGCCTTGCCAGAGGCGCCGAGCCCTTGACATGGAACCCCGCTGCCCCCTGG 60  
DB 38 GGAAGCCTTGCCAGAGGCGCCGAGCCCTTGACATGGAACCCCGCTGCCCCCTGG 97  
QY 61 GAGCTGCAATCTGCGCTTTCTGAGGAGGCTGACCTGGGCGATGCTGTCAGAGGC 120  
DB 98 GAGCTGCAATCTGCGCTTTCTGAGGAGGCTGACCTGGGCGATGCTGTCAGAGGC 157  
QY 121 CAACAGAAATACGCGAGATCTGCTCTGCGCCCTAGACTACGACACCTGCGGGCC 180  
DB 158 CAACAGAAATACGCGAGATCTGCTCTGCGCCCTAGACTACGACACCTGCGGGCC 217  
QY 181 TACTTCTCCGTTACTACTACTACAGAGTACAGCAGAGTCTGCGCACTTCTGTACGG 240  
DB 218 TACTTCTCCGTTACTACTACTACAGAGTACAGCAGAGTCTGCGCACTTCTGTACGG 277  
QY 241 GCTGCGAGGCGAAGCGCAAACTTTCTACACTGCGGAGGCTTGGACGATGCTTGTGCTGA 300  
DB 278 GCTGCGAGGCGAAGCGCAAACTTTCTACACTGCGGAGGCTTGGACGATGCTTGTGCTGA 337  
QY 301 GGAATGAAAAAGTCCCAAGTTTGCCGCTGCAAGTACGATGAGTGAAG 360  
DB 338 GGAATGAAAAAGTCCCAAGTTTGCCGCTGCAAGTACGATGAGTGAAG 397  
QY 361 GGTCCACAGAAAAATTTCTTTAATCTAAGTTCCATGACATGTAATAATCTTTTCG 420  
DB 398 GGTCCACAGAAAAATTTCTTTAATCTAAGTTCCATGACATGTAATAATCTTTTCG 457  
QY 421 GTGGGTGCACCGGAACCGGATTTGAGAACGGTTTCCAGTAGACTCTGTATAGGGCT 480  
DB 458 GTGGGTGCACCGGAACCGGATTTGAGAACGGTTTCCAGTAGACTCTGTATAGGGCT 517  
QY 481 TCTGCGCACCAAGAAATTTCCATCTTTGCTACAGTCCAAAGATGAGGAGCTGTGCT 540  
DB 518 TCTGCGCACCAAGAAATTTCCATCTTTGCTACAGTCCAAAGATGAGGAGCTGTGCT 577  
QY 541 CTGCGAATGTGACTGCTATTTTAACTTTAATCAAGATACAGAACTGTGATGCTTCACTT 600  
DB 578 CTGCGAATGTGACTGCTATTTTAACTTTAATCAAGATACAGAACTGTGATGCTTCACTT 637  
QY 601 ATACTGGCTGAGGAGGAAATGCAATCTTTGTTAGAGGAGGATTTGCAAAAGTGCAT 660  
DB 638 ATACTGGCTGAGGAGGAAATGCAATCTTTGTTAGAGGAGGATTTGCAAAAGTGCAT 697  
QY 661 GTGCAAAAGCTTTGAAAAAGAAAGATGCAAGCTTGCCTTGCAGTAGAATCC 720  
DB 698 GTGCAAAAGCTTTGAAAAAGAAAGATGCAAGCTTGCCTTGCAGTAGAATCC 757

Query Match 100.0%; Score 979; DB 9; Length 1203;  
Best Local Similarity 100.0%; Pred. No. 3,1e-247;  
Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 GGAGCGCTTGGCCGAGCGGCGCGCCGCTGCAACATGAGCCCGCTGCGCCCTGG 60  
Db 38 GGAGCGCTTGGCCGAGCGGCGCGCCGCTGCAACATGAGCCCGCTGCGCCCTGG 97

Query 61 GGCTGTGATTCGTGCTGCTTTCCTGAGGAGGCTGCACTGCGGAGTGTCTCAGAGC 120  
Db 98 GGCTGTGATTCGTGCTGCTTTCCTGAGGAGGCTGCACTGCGGAGTGTCTCAGAGC 157

Query 121 CAACAGAAATTAACGCGAGATCTGTCTCTGCGCCCTAGACTACGAGACCTGCGGCGCC 180  
Db 158 CAACAGAAATTAACGCGAGATCTGTCTCTGCGCCCTAGACTACGAGACCTGCGGCGCC 217

Query 181 TACTTCTCCGTTACTACTACGAGAGTACGCGAGAGCTGCGCGCACTTCTGTAAGG 240  
Db 218 TACTTCTCCGTTACTACTACGAGAGTACGCGAGAGCTGCGCGCACTTCTGTAAGG 277

Query 241 GCTGAGAGGCAAGCGCAATTTCTACACTGAGAGGCTTGCACATGCTTCTGTA 300  
Db 278 GCTGAGAGGCAAGCGCAATTTCTACACTGAGAGGCTTGCACATGCTTCTGTA 337

Query 301 GGAATGAAAAAGTTCCCAAGTTTCCGCGCTCAAGTAGTGTGACGACGAGTGTGAGG 360  
Db 338 GGAATGAAAAAGTTCCCAAGTTTCCGCGCTCAAGTAGTGTGACGACGAGTGTGAGG 397

Query 361 GGTCCACAGAAAAAGTATTTCTTAAATCTAAGTTCAGATGTAAGAAAAATTTCTTCCG 420  
Db 398 GGTCCACAGAAAAAGTATTTCTTAAATCTAAGTTCAGATGTAAGAAAAATTTCTTCCG 457

Query 421 GTGGGTGTCAACGGAAACCGGATTTGAGAACAGGTTTCCAGATGAACTACTGTATGGCT 480

RESULT 6  
US-10-991-321-23  
Sequence 23, Application US/10991321  
Publication No. US20050112675A1  
GENERAL INFORMATION:  
APPLICANT: Kochen, Jarema Peter  
APPLICANT: Rosinski, James Andrew  
TITLE OF INVENTION: Specific Markers for Metabolic Syndrome  
FILE REFERENCE: 21742 US1  
CURRENT APPLICATION NUMBER: US/10/991,321  
CURRENT FILING DATE: 2004-11-17  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 23  
LENGTH: 1203  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-991-321-23

Query Match 100.0%; Score 979; DB 9; Length 1203;  
Best Local Similarity 100.0%; Pred. No. 3,1e-247;  
Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 GGAGCGCTTGGCCGAGCGGCGCGCCGCTGCAACATGAGCCCGCTGCGCCCTGG 60  
Db 38 GGAGCGCTTGGCCGAGCGGCGCGCCGCTGCAACATGAGCCCGCTGCGCCCTGG 97

Query 61 GGCTGTGATTCGTGCTGCTTTCCTGAGGAGGCTGCACTGCGGAGTGTCTCAGAGC 120  
Db 98 GGCTGTGATTCGTGCTGCTTTCCTGAGGAGGCTGCACTGCGGAGTGTCTCAGAGC 157

Query 121 CAACAGAAATTAACGCGAGATCTGTCTCTGCGCCCTAGACTACGAGACCTGCGGCGCC 180  
Db 158 CAACAGAAATTAACGCGAGATCTGTCTCTGCGCCCTAGACTACGAGACCTGCGGCGCC 217

Query 181 TACTTCTCCGTTACTACTACGAGAGTACGCGAGAGCTGCGCGCACTTCTGTAAGG 240  
Db 218 TACTTCTCCGTTACTACTACGAGAGTACGCGAGAGCTGCGCGCACTTCTGTAAGG 277

Query 241 GCTGAGAGGCAAGCGCAATTTCTACACTGAGAGGCTTGCACATGCTTCTGTA 300  
Db 278 GCTGAGAGGCAAGCGCAATTTCTACACTGAGAGGCTTGCACATGCTTCTGTA 337

Query 301 GGAATGAAAAAGTTCCCAAGTTTCCGCGCTCAAGTAGTGTGACGACGAGTGTGAGG 360  
Db 338 GGAATGAAAAAGTTCCCAAGTTTCCGCGCTCAAGTAGTGTGACGACGAGTGTGAGG 397

Query 361 GGTCCACAGAAAAAGTATTTCTTAAATCTAAGTTCAGATGTAAGAAAAATTTCTTCCG 420  
Db 398 GGTCCACAGAAAAAGTATTTCTTAAATCTAAGTTCAGATGTAAGAAAAATTTCTTCCG 457

Query 421 GTGGGTGTCAACGGAAACCGGATTTGAGAACAGGTTTCCAGATGAACTACTGTATGGCT 480

RESULT 7  
US-09-814-353-19662  
Sequence 19662, Application US/09814353  
Publication No. US20030165831A1  
GENERAL INFORMATION:  
APPLICANT: Thompson, Pamela  
APPLICANT: Lee, John  
APPLICANT: Lillie, James  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR  
IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
THERAPY OF OVARIAN CANCER  
FILE REFERENCE: MRI-006B  
CURRENT APPLICATION NUMBER: US/09/814,353  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: US 60/191,031  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: US 60/207,124  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: US 60/211,940  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: US 60/216,820  
PRIOR FILING DATE: 2000-07-07  
PRIOR APPLICATION NUMBER: US 60/220,661  
PRIOR FILING DATE: 2000-07-25  
PRIOR APPLICATION NUMBER: US 60/257,672  
PRIOR FILING DATE: 2000-12-21  
NUMBER OF SEQ ID NOS: 22037  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 19662  
LENGTH: 2407  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-814-353-19662

Query Match 100.0%; Score 979; DB 3; Length 2407;  
Best Local Similarity 100.0%; Pred. No. 4,7e-247;  
Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GGAAGCCCTTGGCCGAGCGGCGCGCCGAGACCCCTGACATGAGACCCGCTGCGCCCTCG 60  
74 GAGCCCTTGGCCGAGCGGCGCGCCGAGACCCCTGACATGAGACCCGCTGCGCCCTCG 133  
61 GAGCTGCAATTCGTGCTTCTTCTGACGAGAGCTGCACTGGGCGATGCTGCTCAGAGC 120  
134 GAGCTGCAATTCGTGCTTCTTCTGACGAGAGCTGCACTGGGCGATGCTGCTCAGAGC 193  
121 CAACGGAATTAACCGGAGATCTGTCTCTGCGCCCTGAGACTACGAGCCCTGCGGCGCC 180  
194 CAACGGAATTAACCGGAGATCTGTCTCTGCGCCCTGAGACTACGAGCCCTGCGGCGCC 253  
181 TACTCTCCGTTACTACTACGAGGTAACGAGTACGAGGCTGCGGAGTCTGTTACGAGG 240  
254 TACTCTCCGTTACTACTACGAGGTAACGAGTACGAGGCTGCGGAGTCTGTTACGAGG 313  
241 GCTGCGAGGCGCAACGCAATTTCTACACTGGAGGCTTGGCAGATGCTTGGTGA 300  
314 GCTGCGAGGCGCAACGCAATTTCTACACTGGAGGCTTGGCAGATGCTTGGTGA 373  
301 GGAATGAAAAAGTTCCCAAGTTTCCGCTGCAAGTGAAGTGAACAACGATGAGG 360  
374 GGAATGAAAAAGTTCCCAAGTTTCCGCTGCAAGTGAAGTGAACAACGATGAGG 433  
351 GGTCCACAGAAAAAGTATTTCTTAATCTAAGTTCAGATGCAAGTGAAGAAAAATCTTTTCCG 420  
434 GGTCCACAGAAAAAGTATTTCTTAATCTAAGTTCAGATGCAAGTGAAGAAAAATCTTTTCCG 493  
421 GTGGGTGTACCGGAAACCGGATGGAACAAGTTTCCAGATGAGACTTGTATGGCT 480  
494 GTGGGTGTACCGGAAACCGGATGGAACAAGTTTCCAGATGAGACTTGTATGGCT 553  
481 TGTGGGCACCAAGAAAAATTCATCAATTTTGTCTACAGTCCAAAGATGAGGAGCTGTGCT 540  
554 TGTGGGCACCAAGAAAAATTCATCAATTTTGTCTACAGTCCAAAGATGAGGAGCTGTGCT 613  
541 CTGGCAATGTGACTCGCTAATTTTAAATTCAGAGTACAGAACTGTATGCTTCACT 600  
614 CTGGCAATGTGACTCGCTAATTTTAAATTCAGAGTACAGAACTGTATGCTTCACT 673  
601 ATACTGCTGTGAGGGAATGACATACTTGTGAGGAGGATGCAACGCTGAT 660  
674 ATACTGCTGTGAGGGAATGACATACTTGTGAGGAGGATGCAACGCTGAT 733  
661 GTGCAAAAGCTTTGAAAAAGAAAGATGCGCAAGCTTGGCTTGGCAGTGAATCC 720  
734 GTGCAAAAGCTTTGAAAAAGAAAGATGCGCAAGCTTGGCTTGGCAGTGAATCC 793  
721 GGAATAATTCGGAAGAAAGATTTTAAACATTTTAAATGATGATGTTGTGCTTAAAG 780  
794 GGAATAATTCGGAAGAAAGATTTTAAACATTTTAAATGATGATGTTGTGCTTAAAG 853  
781 GCTAATTTGCTTAAATGTTGATCTGAAGATATATATGACAGTGAAGAAACAATCA 840  
854 GCTAATTTGCTTAAATGTTGATCTGAAGATATATATGACAGTGAAGAAACAATCA 913  
841 TTGGTGAATTAATTCACGATTTTAAATTAATACAGTCACTTTTCAAAAAATTTGATTTT 900  
914 TTGGTGAATTAATTCACGATTTTAAATTAATACAGTCACTTTTCAAAAAATTTGATTTT 973  
901 TTATATATTAATTAATGCTGCTAATCAAAATGATGATACATTTTAAATTAATGTTGAC 960  
974 TTATATATTAATTAATGCTGCTAATCAAAATGATGATGATACATTTTAAATTAATGTTGAC 1033  
961 TGTGTGTGAGACTGAATTC 979  
1034 TGTGTGTGAGACTGAATTC 1052

RESULT 8  
US-10-044-090-609  
; Sequence 609, Application US/10044090  
; Publication No. US20020137081A1  
; GENERAL INFORMATION:  
; APPLICANT: Oiga Bandman  
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION  
; FILE REFERENCE: PA-0028 US  
; CURRENT APPLICATION NUMBER: US/10/044, 090  
; CURRENT FILING DATE: 2002-01-09  
; NUMBER OF SEQ ID NOS: 850  
; SOFTWARE: PERL Program  
; SEQ ID NO 609  
; LENGTH: 2540  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20020137081A1 181172CB1  
US-10-044-090-609

Query Match 100.0%; Score 979; DB 5; Length 2540;

Best Local Similarity 100.0%; Pred. No. 4,8e-247;  
Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GGAAGCCCTTGGCCGAGCGGCGCGCCGAGACCCCTGACACATGAGACCCGCTGCGCCCTCG 60  
27 GAGCCCTTGGCCGAGCGGCGCGCCGAGACCCCTGACACATGAGACCCGCTGCGCCCTCG 86  
61 GAGCTGCAATTCGTGCTTCTTCTGACGAGAGCTGCACTGGGCGATGCTGCTCAGAGC 120  
87 GAGCTGCAATTCGTGCTTCTTCTGACGAGAGCTGCACTGGGCGATGCTGCTCAGAGC 146  
121 CAACGGAATTAACCGGAGATCTGTCTCTGCGCCCTGAGACTACGAGCCCTGCGGCGCC 180  
147 CAACGGAATTAACCGGAGATCTGTCTCTGCGCCCTGAGACTACGAGCCCTGCGGCGCC 206  
181 TACTCTCCGTTACTACTACGAGGTAACGAGTACGAGGCTGCGGAGTCTGTTACGAGG 240  
207 TACTCTCCGTTACTACTACGAGGTAACGAGTACGAGGCTGCGGAGTCTGTTACGAGG 266  
241 GCTGCGAGGCGCAACGCAATTTCTACACTGGAGGCTTGGCAGATGCTTGGTGA 300  
267 GCTGCGAGGCGCAACGCAATTTCTACACTGGAGGCTTGGCAGATGCTTGGTGA 326  
301 GGAATGAAAAAGTTCCCAAGTTTCCGCTGCAAGTGAAGTGAACAACGATGAGG 360  
327 GGAATGAAAAAGTTCCCAAGTTTCCGCTGCAAGTGAAGTGAACAACGATGAGG 386  
361 GGTCCACAGAAAAAGTATTTCTTAATCTAAGTTCATGACATGTAAGAAAAATCTTTTCCG 420  
387 GGTCCACAGAAAAAGTATTTCTTAATCTAAGTTCATGACATGTAAGAAAAATCTTTTCCG 446  
421 GTGGGTGTACCGGAAACCGGATGGAACAAGTTTCCAGATGAGACTTGTATGGCT 480  
447 GTGGGTGTACCGGAAACCGGATGGAACAAGTTTCCAGATGAGACTTGTATGGCT 506  
481 TGTGCGACCAAGAAAAATTCATCAATTTTGTCTACAGTCCAAAGATGAGGAGCTGTGCT 540  
507 TGTGCGACCAAGAAAAATTCATCAATTTTGTCTACAGTCCAAAGATGAGGAGCTGTGCT 566  
541 CTGGCAATGTGACTCGCTAATTTTAAATTCAGAGTACAGAACTGTATGCTTCACT 600  
567 CTGGCAATGTGACTCGCTAATTTTAAATTCAGAGTACAGAACTGTATGCTTCACT 626  
601 ATACTGCTGTGAGGGAATGACATACTTGTGAGGAGGATGCAACGCTGAT 660  
627 ATACTGCTGTGAGGGAATGACATACTTGTGAGGAGGATGCAACGCTGAT 686  
661 GTGCAAAAGCTTTGAAAAAGAAAGATGCGCAAGCTTGGCTTGGCAGTGAATCC 720  
687 GTGCAAAAGCTTTGAAAAAGAAAGATGCGCAAGCTTGGCTTGGCAGTGAATCC 746

Qy 721 GGAATAATCGAAGAGCAATTTTAACATCTTAATATGTCATCTGTTGCTTTTANG 780  
Db 747 GGAATAATCGAAGAGCAATTTTAACATCTTAATATGTCATCTGTTGCTTTTANG 806  
Qy 781 GCTTATTTGCTTTATGTTGATCTGAGATTAATATGACAGATGAGAAACAATCA 840  
Db 807 GCTTATTTGCTTTATGTTGATCTGAGATTAATATGACAGATGAGAAACAATCA 866  
Qy 841 TTGGGATTTATTCACCGCTTTTATTAATACAGTCACTTTTCAAAAATTTGATTTT 900  
Db 867 TTGGGATTTATTCACCGCTTTTATTAATACAGTCACTTTTCAAAAATTTGATTTT 926  
Qy 901 TTATATATTAATCTAGCTGATTAATGAAATGAGTGTACATTTTAAATTTATGTTTAAAC 960  
Db 927 TTATATATTAATCTAGCTGATTAATGAAATGAGTGTACATTTTAAATTTATGTTTAAAC 986  
Qy 961 TGTGTTGAGACTGAAATTC 979  
Db 987 TGTGTTGAGACTGAAATTC 1005

## RESULT 9

US-10-084-817-143  
Sequence 143, Application US/10084817  
Publication No. US20030119009A1  
GENERAL INFORMATION:  
APPLICANT: Susan Stewart  
APPLICANT: Jed G. Nuchtern  
APPLICANT: Sharon E. Pion  
APPLICANT: Jason M. Shohet  
TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION  
FILE REFERENCE: PA-0046 US  
CURRENT APPLICATION NUMBER: US/10/084,817  
CURRENT FILING DATE: 2002-02-25  
PRIOR APPLICATION NUMBER: 60/270,784  
PRIOR FILING DATE: 2001-02-23  
NUMBER OF SEQ ID NOS: 365  
SOFTWARE: PERL Program  
SEQ ID NO 143  
LENGTH: 2540  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: msc\_feature  
OTHER INFORMATION: Incyte ID No. US20030119009A1 181172CBI  
US-10-084-817-143

Query Match 100.0%; Score 979; DB 5; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 4,88-247;  
Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCGCTTGGCCAGCGGGCGCGCCGACCCCTGACATGAGACCCGCTCGCCCTGG 60  
Db 27 GGAAGCGCTTGGCCAGCGGGCGCGCCGACCCCTGACATGAGACCCGCTCGCCCTGG 86  
Qy 61 GCGTGTGATTTCTGCTCTTTTCTGACGAGAGCTGCACTGGGCGATGCTGCTGAGAGC 120  
Db 87 GCGTGTGATTTCTGCTCTTTTCTGACGAGAGCTGCACTGGGCGATGCTGCTGAGAGC 146  
Qy 121 CAACGAGAAATPAGCGGAGATCTGCTCTGCGCCCTGAGACTAGAGGAGCCCTGCGGGGCC 180  
Db 147 CAACGAGAAATPAGCGGAGATCTGCTCTGCGCCCTGAGACTAGAGGAGCCCTGCGGGGCC 206  
Qy 181 TACTTCTCGTTACTACTACGACAGTACACGACAGAGCTGCGGCAAGTTCTGTAAGGAG 240  
Db 207 TACTTCTCGTTACTACTACGACAGTACACGACAGAGCTGCGGCAAGTTCTGTAAGGAG 266  
Qy 241 GCTGAGAGGCGAAGCGCAATTTTCTACACCTGAGAGGCTTGGACAGATGCTTCTGGA 300  
Db 267 GCTGAGAGGCGAAGCGCAATTTTCTACACCTGAGAGGCTTGGACAGATGCTTCTGGA 326  
Qy 301 GGATGAGAAAGTTGCCAAAGTTTCCGGCTGCAAGTAGTGTGACGACAGTGTGAGG 360

RESULT 10  
US-10-097-340-315  
Sequence 315, Application US/10097340  
Publication No. US20030087250A1

GENERAL INFORMATION:  
APPLICANT: John MONAHAN  
APPLICANT: Manjula GANNAVABU  
APPLICANT: Sebastian HORSCH  
APPLICANT: Shubhangi KAMATKAR  
APPLICANT: Steve G. KOVATS  
APPLICANT: Rachel E. MEYERS  
APPLICANT: Michael MORRISSEY  
APPLICANT: Peter OLANDT  
APPLICANT: Ami SEN  
APPLICANT: Peter VEIBY  
APPLICANT: Gordon B. MILLS  
APPLICANT: Robert C. BAST, Jr.  
APPLICANT: Karen LU  
APPLICANT: Rosemarie SCHMANDT  
APPLICANT: Xumei ZHAO  
APPLICANT: Karen GLATT  
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins for The Identification,  
FILE REFERENCE: MRI-030  
CURRENT APPLICATION NUMBER: US/10/097,340



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/ CURRENT FILING DATE: 2002-03-14
/ PRIOR APPLICATION NUMBER: 60/276,025
/ PRIOR FILING DATE: 2001-03-14
/ PRIOR APPLICATION NUMBER: 60/325,149
/ PRIOR FILING DATE: 2001-09-26
/ PRIOR APPLICATION NUMBER: 60/276,026
/ PRIOR FILING DATE: 2001-03-14
/ PRIOR APPLICATION NUMBER: 60/324,967
/ PRIOR FILING DATE: 2001/09/26
/ PRIOR APPLICATION NUMBER: 60/311,732
/ PRIOR FILING DATE: 2001-08-10
/ PRIOR APPLICATION NUMBER: 60/325,102
/ PRIOR FILING DATE: 2001-09-26
/ PRIOR APPLICATION NUMBER: 60/323,580
/ PRIOR FILING DATE: 2001-09-19
/ NUMBER OF SEQ ID NOS: 363
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 315
/ LENGTH: 1142
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-097-340-315
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Query Match 99.3%; Score 972.2; DB 5; Length 1142;

Best Local Similarity 99.7%; Pred. No. 1.9e-245; Matches 974; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 GGAGCCCTTGGCCAGCGGCGCGCCGAGCCCTGACACATGAGACCCCGCTGCGCCCTGCG 60
DB 19 GGAAGCCCTTGGCCAGCGGCGCGCGCCGAGCCCTGACACATGAGACCCCGCTGCGCCCTGCG 78
QY 61 GCGCTCGATTCTGCTGCTTTTCTGACGAGGCTGCACTGGGCGATGCTGCTCAGAGAC 120
DB 79 GCGCTCGATTCTGCTGCTTTTCTGACGAGGCTGCACTGGGCGATGCTGCTCAGAGAC 138
QY 121 CAACGAGAAATACCGGAGATCTCTCCCTGAGCTAGACGAGACCTGCGCGGCGCC 180
DB 139 CAACGAGAAATACCGGAGATCTCTCTCCCTGAGCTAGACGAGACCTGCGCGGCGCC 198
QY 181 TACTTCTCCGTTACTACTACGACAGATACACGACAGAGCTGCGCGAGTTCTGTACGGGG 240
DB 199 TACTTCTCCGTTACTACTACGACAGATACACGACAGAGCTGCGCGAGTTCTGTACGGGG 258
QY 241 GCTGCGAGGGCAACCGCAAACTTTCTACCTGAGAGGCTTGCAGACATGCTTGCGA 300
DB 259 GCTGCGAGGGCAACCGCAAACTTTCTACCTGAGAGGCTTGCAGACATGCTTGCGA 318
QY 301 GGAATGAAAAGTTCCCAAGTTTGGCGCTGCAAGTGAAGTGAACAACGATGTGAGG 360
DB 319 GGAATGAAAAGTTCCCAAGTTTGGCGCTGCAAGTGAAGTGAACAACGATGTGAGG 378
QY 361 GGTCCACAGAAAAGTATTTCTTAATCTAAGTTCATGACATGTAAGAAAATTTCTTTCCG 420
DB 379 GGTCCACAGAAAAGTATTTCTTAATCTAAGTTCATGACATGTAAGAAAATTTCTTTCCG 438
QY 421 GTGGGTGTCACCGGAAACCGGATGAGAAACAGGTTTCCAGATGAACCTTGTATGGGCT 480
DB 439 GTGGGTGTCACCGGAAACCGGATGAGAAACAGGTTTCCAGATGAACCTTGTATGGGCT 498
QY 481 TCTGGGCAACAAAGAAATTCATGATTTTGTCTAAGTCCAAAGAAATGAGGGAGCTGTGCT 540
DB 499 TCTGGGCAACAAAGAAATTCATGATTTTGTCTAAGTCCAAAGAAATGAGGGAGCTGTGCT 558
QY 541 CTGCAATGTGACTGCTATTTTAAATCCAAAGATAGAGAACTGTGATGCTTCACTT 600
DB 559 CTGCAATGTGACTGCTATTTTAAATCCAAAGATAGAGAACTGTGATGCTTCACTT 618
QY 601 ATACTGCTGTGAGAGGAAATGCAATTAATTTGTTAGAGAGGAGATTGCAAACTGCAT 660
DB 619 ATACTGCTGTGAGAGGAAATGCAATTAATTTGTTAGAGAGGAGATTGCAAACTGCAT 678
QY 661 GTGCAAAAGCTTTGAAAAGAAAAGAAAGATGCCAAAGCTTCCCTTGGCAGTGAATCC 720
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DB 679 GTGCAAAAGCTTTGAAAAGAAAAGAAAGATGCCAAAGCTTCCCTTGGCAGTGAATCC 738
QY 721 GGAATAATCGAGAGAGCAATTTTAAACATTTAATATGATCATCTTGTGCTTTATG 780
DB 739 GGAATAATCGAGAGAGCAATTTTAAACATTTAATATGATCATCTTGTGCTTTATG 798
QY 781 GCTTATTTGCTTTATGTTGTATCTGAAAGATTAATATGACATGAGAGAAACAAATCA 840
DB 799 GCTTATTTGCTTTATGTTGTATCTGAAAGATTAATATGACATGAGAGAAACAAATCA 858
QY 841 TTGGGATTTATTCACGAGTTTATTTAATTAATCAAGTCACTTTTCAAAAATTTGATTTT 900
DB 859 TTGGGATTTATTCACGAGTTTATTTAATTAATCAAGTCACTTTTCAAAAATTTGATTTT 918
QY 901 TTATATATTAAGTACTGCTATTCATTAATGATGCTTACATTTTAAATTTATGTTCAAC 960
DB 919 TTATATATTAAGTACTGCTATTCATTAATGATGCTTACATTTTAAATTTATGTTCAAC 978
QY 961 TGTTTGTAGACTGAAT 977
DB 979 TGTTTGTAGACTGAAT 995
```

RESULT 11

US-10-021-660-53

/ Sequence 53, Application US/10021660

/ Publication No. US20030152926A1

/ GENERAL INFORMATION:

/ APPLICANT: Glynn, Richard

/ APPLICANT: Watson, Susan R.

/ APPLICANT: EOS Biotechnology, Inc.

/ TITLE OF INVENTION: No. US20030152926A1e1 Methods of Diagnosis of Angiogenesis,

/ TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis

/ FILE REFERENCE: 018501-000710US

/ CURRENT APPLICATION NUMBER: US/10/021,660

/ PRIOR FILING DATE: 2001-12-06

/ PRIOR FILING DATE: 2001-02-14

/ PRIOR APPLICATION NUMBER: US 09/637,977

/ PRIOR FILING DATE: 2000-08-11

/ NUMBER OF SEQ ID NOS: 135

/ SOFTWARE: FastSeq for Windows Version 3.0

/ SEQ ID NO 53

/ LENGTH: 1142

/ TYPE: DNA

/ ORGANISM: Homo sapiens

US-10-021-660-53

Query Match 99.3%; Score 972.2; DB 6; Length 1142;

Best Local Similarity 99.7%; Pred. No. 1.9e-245; Matches 974; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
QY 1 GGAGCCCTTGGCCAGCGGCGCGCCGAGCCCTGACACATGAGACCCCGCTGCGCCCTGCG 60
DB 19 GGAAGCCCTTGGCCAGCGGCGCGCGCCGAGCCCTGACACATGAGACCCCGCTGCGCCCTGCG 78
QY 61 GCGCTCGATTCTGCTGCTTTTCTGACGAGGCTGCACTGGGCGATGCTGCTCAGAGAC 120
DB 79 GCGCTCGATTCTGCTGCTTTTCTGACGAGGCTGCACTGGGCGATGCTGCTCAGAGAC 138
QY 121 CAACGAGAAATACCGGAGATCTGTCTCTGCGCCCTAGACTAGAGACCTGCGCGGCGCC 180
DB 139 CAACGAGAAATACCGGAGATCTGTCTCTGCGCCCTAGACTAGAGACCTGCGCGGCGCC 198
QY 181 TACTTCTCCGTTACTACTACGACAGATACACGACAGAGCTGCGCGAGTTCTGTACGGGG 240
DB 199 TACTTCTCCGTTACTACTACGACAGATACACGACAGAGCTGCGCGAGTTCTGTACGGGG 258
QY 241 GCTGCGAGGGCAACCGCAAACTTTCTACCTGAGAGGCTTGCAGACATGCTTGCGA 300
DB 259 GCTGCGAGGGCAACCGCAAACTTTCTACCTGAGAGGCTTGCAGACATGCTTGCGA 318
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QY 301 GGATGAAAAAGTTCCCAAGTTTCCCGCTGCAGTGAAGTGGACGACGAGTGTAGG 360  
DB 319 GGATGAAAAAGTTCCCAAGTTTCCCGCTGCAGTGAAGTGGACGACGAGTGTAGG 378  
QY 361 GGTCCACAGAAAAGTATTTCTTAATCTAAGTTCAGTACATGTGAAAAATTTCTTTCCG 420  
DB 379 GGTCCACAGAAAAGTATTTCTTAATCTAAGTTCAGTACATGTGAAAAATTTCTTTCCG 438  
QY 421 GTGGGTGTACCGGAAACCGGATTTGAAACAGGTTTCCAGTGAAGCTATGTATGGCT 480  
DB 439 GTGGGTGTACCGGAAACCGGATTTGAAACAGGTTTCCAGTGAAGCTATGTATGGCT 498  
QY 481 TCTGGGCAACCAAGAAAATTCATCTATTTGTCTAAGTCCAAAGATAGAGGACGTGTCT 540  
DB 499 TCTGGGCAACCAAGAAAATTCATCTATTTGTCTAAGTCCAAAGATAGAGGACGTGTCT 558  
QY 541 CTGCCAATGTGACTGCTATTTATTTAATCCAGATAGAGAACTGTATGCTTCACT 600  
DB 559 CTGCCAATGTGACTGCTATTTATTTAATCCAGATAGAGAACTGTATGCTTCACT 618  
QY 601 ATACTGCTGTGAGAGGAATGCAATTAATTTTGAAGAGGAGATTGCAACGTGCAT 660  
DB 619 ATACTGCTGTGAGAGGAATGCAATTAATTTTGAAGAGGAGATTGCAACGTGCAT 678  
QY 661 GTGCAAAAGCTTTGAAAAAGAAAAGAGATGCCAAAGCTTGTGCTTCCAGTAAATCC 720  
DB 679 GTGCAAAAGCTTTGAAAAAGAAAAGAGATGCCAAAGCTTGTGCTTCCAGTAAATCC 738  
QY 721 GGAATAATTCGGAAGAAAGATTTTAAACATTTCTAATATGTCTATTTGTCTTTTNG 780  
DB 739 GGAATAATTCGGAAGAAAGATTTTAAACATTTCTAATATGTCTATTTGTCTTTTNG 798  
QY 781 GCTTATTTGCTTTTNGGTTGTATCTGAAGAAATTAATGACAGATGAGAAAACAAATCA 840  
DB 799 GCTTATTTGCTTTTNGGTTGTATCTGAAGAAATTAATGACAGATGAGAAAACAAATCA 858  
QY 841 TTGGGATTTTATTCACAGTTTATTTAATTAACAATCTTTTGAATAATTTGATTTT 900  
DB 859 TTGGGATTTTATTCACAGTTTATTTAATTAACAATCTTTTGAATAATTTGATTTT 918  
QY 901 TTATATATTAATTAAGTCTGATTTCAATGTGAGTACAAATTTAATTAATGTTCAC 960  
DB 919 TTATATATTAATTAAGTCTGATTTCAATGTGAGTACAAATTTAATTAATGTTCAC 978  
QY 961 TGTTTGTGAGACTGAAT 977  
DB 979 TGTTTGTGAGACTGAAT 995

RESULT 12  
US-10-295-027-23  
Sequence 23, Application US/10295027  
Publication No. US2003023250A1  
GENERAL INFORMATION:  
APPLICANT: Afar, Daniel  
APPLICANT: Aziz, Natsaba  
APPLICANT: Gineberg, Wendy M.  
APPLICANT: Gish, Kurt C.  
APPLICANT: Glyne, Richard  
APPLICANT: Hevez, Peter A.  
APPLICANT: Mack, David H.  
APPLICANT: Murray, Richard  
APPLICANT: Watson, Susan R.  
APPLICANT: Eos Biotechnology, Inc.  
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and  
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer  
FILE REFERENCE: 018501-012500US  
CURRENT APPLICATION NUMBER: US/10/295,027  
CURRENT FILING DATE: 2002-11-13  
PRIOR APPLICATION NUMBER: US 09/663,733  
PRIOR FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: US 60/350,666

QY PRIOR FILING DATE: 2001-11-13  
DB PRIOR APPLICATION NUMBER: US 60/335,394  
QY PRIOR FILING DATE: 2001-11-15  
DB PRIOR APPLICATION NUMBER: US 60/332,464  
QY PRIOR FILING DATE: 2001-11-21  
DB PRIOR APPLICATION NUMBER: US 60/334,393  
QY PRIOR FILING DATE: 2001-11-29  
DB PRIOR APPLICATION NUMBER: US 60/340,376  
QY PRIOR FILING DATE: 2001-12-14  
DB PRIOR APPLICATION NUMBER: US 60/347,211  
QY PRIOR FILING DATE: 2002-01-08  
DB PRIOR APPLICATION NUMBER: US 60/347,349  
QY PRIOR FILING DATE: 2002-01-10  
DB PRIOR APPLICATION NUMBER: US 60/355,250  
QY PRIOR FILING DATE: 2002-02-08  
DB PRIOR APPLICATION NUMBER: US 60/356,714  
QY Remaining Prior Application data removed - See File Wrapper or PALM.  
DB NUMBER OF SEQ ID NOS: 1386  
QY SOFTWARE: PatentIn Ver. 2.1  
DB SEQ ID NO 23  
QY LENGTH: 1142  
DB TYPE: DNA  
QY ORGANISM: Homo sapiens  
DB US-10-295-027-23

Query Match 99.3%; Score 972.2; DB 6; Length 1142;  
Best Local Similarity 99.7%; Pred. No. 1.9e-245;  
Matches 974; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAGAGCTTGGCCAGAGCGGCGCCGACCCCTGACATGAGAACCCGCTGCGCCCTG 60  
DB 19 GAGAGCTTGGCCAGAGCGGCGCCGACCCCTGACATGAGAACCCGCTGCGCCCTG 78  
QY 61 GAGTGTGATTTCTGTGCTTTTCTGAGAGGCTGCACTGAGGCTGCTGCTGAGAGC 120  
DB 79 GAGTGTGATTTCTGTGCTTTTCTGAGAGGCTGCACTGAGGCTGCTGCTGAGAGC 138  
QY 121 CAACAGAAATTAAGCGGAGATCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
DB 139 CAACAGAAATTAAGCGGAGATCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 198  
QY 181 TACTTCTGCTTACTACTACAGACAGTACAGACAGAGCTGCGCAGTCTGCTGCTGAGG 240  
DB 199 TACTTCTGCTTACTACTACAGACAGTACAGACAGAGCTGCGCAGTCTGCTGCTGAGG 258  
QY 241 GCTGGAAGGCAACGCAATTTCTACCTGAGAGGCTTGCAGAGATGCTGCTGAG 300  
DB 259 GCTGGAAGGCAACGCAATTTCTACCTGAGAGGCTTGCAGAGATGCTGCTGAG 318  
QY 301 GGATGAAAAAGTTCCCAAGTTTCCCGCTGCAGTGAAGTGGACGACGAGTGTAGG 360  
DB 319 GGATGAAAAAGTTCCCAAGTTTCCCGCTGCAGTGAAGTGGACGACGAGTGTAGG 378  
QY 361 GGTCCACAGAAAAGTATTTCTTAATCTAAGTTCAGTACATGTGAAAAATTTCTTTCCG 420  
DB 379 GGTCCACAGAAAAGTATTTCTTAATCTAAGTTCAGTACATGTGAAAAATTTCTTTCCG 438  
QY 421 GTGGGTGTACCGGAAACCGGATTTGAAACAGGTTTCCAGTGAAGCTATGTATGGCT 480  
DB 439 GTGGGTGTACCGGAAACCGGATTTGAAACAGGTTTCCAGTGAAGCTATGTATGGCT 498  
QY 481 TCTGGGCAACCAAGAAAATTCATCTATTTGTCTAAGTCCAAAGATAGAGGACGTGTCT 540  
DB 499 TCTGGGCAACCAAGAAAATTCATCTATTTGTCTAAGTCCAAAGATAGAGGACGTGTCT 558  
QY 541 CTGCCAATGTGACTGCTATTTATTTAATCCAGATAGAGAACTGTATGCTTCACT 600  
DB 559 CTGCCAATGTGACTGCTATTTATTTAATCCAGATAGAGAACTGTATGCTTCACT 618  
QY 601 ATACTGCTGTGAGAGGAATGCAATTAATTTTGAAGAGGAGATTGCAACGTGCAT 660  
DB 619 ATACTGCTGTGAGAGGAATGCAATTAATTTTGAAGAGGAGATTGCAACGTGCAT 678



SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 51  
LENGTH: 1142  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-211-462-51

Query Match 99.3%; Score 972.2; DB 7; Length 1142;  
Beet Local Similarity 99.7%; Pred. No. 1.9e-245;  
Matches 974; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 GGAGCGCTTGGCCAGCGGGCCGCGACCCCTGACACATGAGACCCCGCTGCGCCCTCG 60
DB 19 GGAGCGCTTGGCCAGCGGGCCGCGACCCCTGACACATGAGACCCCGCTGCGCCCTCG 78
QY 61 GGGCTGCGATTCGTGCTTTTCTGACGAGAGCTGCACTGGCGCATGCTGCTCAGAGC 120
DB 79 GGGCTGCGATTCGTGCTTTTCTGACGAGAGCTGCACTGGCGCATGCTGCTCAGAGC 138
QY 121 CAACGAGAAATTAACGGGAGATCTGTCTCTGCGCCCTGACATGAGACCCCGCGGCC 180
DB 139 CAACGAGAAATTAACGGGAGATCTGTCTCTGCGCCCTGACATGAGACCCCGCGGCC 198
QY 181 TACTTCTCCGTTACTACGACAGGTACACGACAGCTGCGCGCATGCTGCTCAGAGC 240
DB 199 TACTTCTCCGTTACTACGACAGGTACACGACAGCTGCGCGCATGCTGCTCAGAGC 258
QY 241 GCTGCGAGGGCAACGCAATTTCTACCTGGAGGCTTGGAGCATGCTGCTGCA 300
DB 259 GCTGCGAGGGCAACGCAATTTCTACCTGGAGGCTTGGAGCATGCTGCTGCA 318
QY 301 GGATGAGAAAGTTTCCCAAGTTTCCCGCTGCAAGTGAAGTGAAGCAAGTGAAG 360
DB 319 GGATGAGAAAGTTTCCCAAGTTTCCCGCTGCAAGTGAAGTGAAGCAAGTGAAG 378
QY 361 GGTCCACAGAAAGATTTCTTAATCTAAGTTCATGACATGTAAGAAATTTCTTTCCG 420
DB 379 GGTCCACAGAAAGATTTCTTAATCTAAGTTCATGACATGTAAGAAATTTCTTTCCG 438
QY 421 GTGGGTGTCACCGGAACCGGATTTGAGAACGTTTCCAGATGAGCTTGTATGGCT 480
DB 439 GTGGGTGTCACCGGAACCGGATTTGAGAACGTTTCCAGATGAGCTTGTATGGCT 498
QY 481 TCTGGGCAACCAAGAAATTTCAATCTTGTGTAAGTTCAGAAATGAGGAGCTGTGCT 540
DB 499 TCTGGGCAACCAAGAAATTTCAATCTTGTGTAAGTTCAGAAATGAGGAGCTGTGCT 558
QY 541 CTGCGAATGTGACTGCTATTTTAAATCCAGATGAGAACTGTGATGCTTCACT 600
DB 559 CTGCGAATGTGACTGCTATTTTAAATCCAGATGAGAACTGTGATGCTTCACT 618
QY 601 ATACTGCTGTGAGGAGGATGCAATTAATTTGATGAGGAGGATTTGCAACCTGCA 660
DB 619 ATACTGCTGTGAGGAGGATGCAATTAATTTGATGAGGAGGATTTGCAACCTGCA 678
QY 661 GTGCAAAAGCTTTGAAAAGAAAAGAAAGATGCAAGCTTGGCTTGGCAGTAAATCC 720
DB 679 GTGCAAAAGCTTTGAAAAGAAAAGAAAGATGCAAGCTTGGCTTGGCAGTAAATCC 738
QY 721 GGAATAATTCGAGAAAGCAATTTTAAACATTTCTAATATGTCATCTTGTGCTTTTANG 780
DB 739 GGAATAATTCGAGAAAGCAATTTTAAACATTTCTAATATGTCATCTTGTGCTTTTANG 798
QY 781 GCTTATTTGCTTATTTGTTGATGTAAGAAATTAATGACATGATGAGAAACAAATCA 840
DB 799 GCTTATTTGCTTATTTGTTGATGTAAGAAATTAATGACATGATGAGAAACAAATCA 858
QY 841 TTGGGATTTATTTACCGATTTTATTAATTAAGATCTTTTCAAAAATTTGATTT 900
DB 859 TTGGGATTTATTTACCGATTTTATTAATTAAGATCTTTTCAAAAATTTGATTT 918
QY 901 TTATATATTAACATGCTATTTCAATGATGATGATGATGATTTTAAATTTATGTTTCAAC 960
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DB 919 TTATATATTAACATGCTATTTCAATGATGATGATGATTTTAAATTTATGTTTCAAC 978
QY 961 TGTGTTGAGCTGAT 977
DB 979 TGTGTTGAGCTGAT 995
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RESULT 15  
US-10-956-157-1625

Sequence 1625, Application US/10956157  
Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Mounts, William

TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

FILE REFERENCE: 031896-043000 (AM 101081)

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT FILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARE: Patentin version 3.2

SEQ ID NO 1625

LENGTH: 1142

TYPE: DNA

ORGANISM: Homo sapiens

US-10-956-157-1625

Query Match 99.3%; Score 972.2; DB 9; Length 1142;  
Beet Local Similarity 99.7%; Pred. No. 1.9e-245;  
Matches 974; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 GGAGCGCTTGGCCAGCGGGCCGCGACCCCTGACACATGAGACCCCGCTGCGCCCTCG 60
DB 19 GGAGCGCTTGGCCAGCGGGCCGCGACCCCTGACACATGAGACCCCGCTGCGCCCTCG 78
QY 61 GGGCTGCGATTCGTGCTTTTCTGACGAGAGCTGCACTGGCGCATGCTGCTCAGAGC 120
DB 79 GGGCTGCGATTCGTGCTTTTCTGACGAGAGCTGCACTGGCGCATGCTGCTCAGAGC 138
QY 121 CAACGAGAAATTAACGGGAGATCTGTCTCTGCGCCCTGACATGAGACCCCGCGGCC 180
DB 139 CAACGAGAAATTAACGGGAGATCTGTCTCTGCGCCCTGACATGAGACCCCGCGGCC 198
QY 181 TACTTCTCCGTTACTACGACAGGTACACGACAGCTGCGCGCATGCTGCTCAGAGC 240
DB 199 TACTTCTCCGTTACTACGACAGGTACACGACAGCTGCGCGCATGCTGCTCAGAGC 258
QY 241 GGTCCACAGAAAGATTTCTTAATCTAAGTTCATGACATGTAAGAAATTTCTTTCCG 300
DB 259 GGTCCACAGAAAGATTTCTTAATCTAAGTTCATGACATGTAAGAAATTTCTTTCCG 318
QY 301 GGATGAGAAAGTTTCCCAAGTTTCCCGCTGCAAGTGAAGTGAAGCAAGTGAAG 360
DB 319 GGATGAGAAAGTTTCCCAAGTTTCCCGCTGCAAGTGAAGTGAAGCAAGTGAAG 378
QY 361 GGTCCACAGAAAGATTTCTTAATCTAAGTTCATGACATGTAAGAAATTTCTTTCCG 420
DB 379 GGTCCACAGAAAGATTTCTTAATCTAAGTTCATGACATGTAAGAAATTTCTTTCCG 438
QY 421 GTGGGTGTCACCGGAACCGGATTTGAGAACGTTTCCAGATGAGCTTGTATGGCT 480
DB 439 GTGGGTGTCACCGGAACCGGATTTGAGAACGTTTCCAGATGAGCTTGTATGGCT 498
QY 481 TCTGGGCAACCAAGAAATTTCAATCTTGTGTAAGTTCAGAAATGAGGAGCTGTGCT 540
DB 499 TCTGGGCAACCAAGAAATTTCAATCTTGTGTAAGTTCAGAAATGAGGAGCTGTGCT 558
QY 541 CTGCGAATGTGACTGCTATTTTAAATCCAGATGAGAACTGTGATGCTTCACT 600
DB 559 CTGCGAATGTGACTGCTATTTTAAATCCAGATGAGAACTGTGATGCTTCACT 618
QY 601 ATACTGCTGTGAGGAGGATGCAATTAATTTGATGAGGAGGATTTGCAACCTGCA 660
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Db 619 ATACTGGCTGTGAGGGAATGCAATTAATTGTTAGCAGGAGGATTCGAAACGTGCAT 678
Qy 661 GTGCAAAAGCTTTGAAAAAGAAAGAGATGCAAGCTTGGCTTGGCAGTAGATCC 720
Db 679 GTGCAAAAGCTTTGAAAAAGAAAGAGATGCAAGCTTGGCTTGGCAGTAGATCC 738
Qy 721 GGAATAATCGAAGAGCAATTTTAAACATCTTAATATGTCATCTGTGTGCTTTAAG 780
Db 739 GGAATAATCGAAGAGCAATTTTAAACATCTTAATATGTCATCTGTGTGCTTTAAG 798
Qy 781 GCTTATTTGCCCTTATNGTGTATCTGAAGATATATGACAGCATGAGAAACAATCA 840
Db 799 GCTTATTTGCCCTTATNGTGTATCTGAAGATATATGACAGCATGAGAAACAATCA 858
Qy 841 TTGATGATTTATTCACCAATTTTATTAATACAGTCACTTTTCAAAAATTGGATTT 900
Db 859 TTGATGATTTATTCACCAATTTTATTAATACAGTCACTTTTCAAAAATTGGATTT 918
Qy 901 TTTATATATTAAGCTGCTATTTCAAAAGTGAAGTCTACCATTTTAAATTATGTTCAAC 960
Db 919 TTTATATATTAAGCTGCTATTTCAAAAGTGAAGTCTACCATTTTAAATTATGTTCAAC 978
Qy 961 TGTTTGTGAGACTGAAT 977
Db 979 TGTTTGTGAGACTGAAT 995
```

Search completed: March 11, 2006, 06:24:56  
Job time : 992 secs



QY 279 GCTTGCGACGATGCTTGTCTGAGAGATGAAAAGTTCCCAAGTTCCGCGCTGCAGAGT 338  
DB 241 GCTTGCGACGATGCTTGTCTGAGAGATGAAAAGTTCCCAAGTTCCGCGCTGCAGAGT 300  
QY 339 AGTGGAGACGACAGTGTAGAGGGGTCCAGAAAAGTATTTCTTTAAATCTTAAGTCCAGT 398  
DB 301 AGTGGAGACGACAGTGTAGAGGGGTCCAGAAAAGTATTTCTTTAAATCTTAAGTCCAGT 360  
QY 399 ACATGTGAAAATTTCTTTCCGCTGGGTGTCAACCGGAAACCGAGTTGAGAACAGTTTCCA 458  
DB 361 ACATGTGAAAATTTCTTTCCGCTGGGTGTCAACCGGAAACCGAGTTGAGAACAGTTTCCA 420  
QY 459 GATGAAGCTACTTGTATGTGGCTTCTGCGCACAAGAAAATTCATCATTTTGTCTACAGT 518  
DB 421 GATGAAGCTACTTGTATGTGGCTTCTGCGCACAAGAAAATTCATCATTTTGTCTACAGT 480  
QY 519 CCAAAAAGATGAGGAGCTGTGCTCTGCGCATGTGACCTCGCTATTTATTTTAAATCCAGATAC 578  
DB 481 CCAAAAAGATGAGGAGCTGTGCTCTGCGCATGTGACCTCGCTATTTATTTTAAATCCAGATAC 540  
QY 579 AGAACCTGTGATGCTTCTTCACTATATCTGCTGTGAGAGGATGACATTAATTTGTAGC 638  
DB 541 AGAACCTGTGATGCTTCTTCACTATATCTGCTGTGAGAGGATGACATTAATTTGTAGC 600  
QY 639 AGGAGAGATTGCAACGTGCTCATGTGCAAAAAGCTTTGAAAAAGAAAAGAGATGCCAAG 698  
DB 601 AGGAGAGATTGCAACGTGCTCATGTGCAAAAAGCTTTGAAAAAGAAAAGAGATGCCAAG 660  
QY 699 CTTCGCTTGGCAGTAGATCCGGAATAATCGGAAGAACATTTTAA 746  
DB 661 CTTCGCTTGGCAGTAGATCCGGAATAATCGGAAGAACATTTTAA 708

## RESULT 2

US-10-310-914A-5835  
Sequence 5835, Application US/10310914A  
Publication No. US20060003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shiller, Kiyuzat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
FILE REFERENCE: 06087, 0200, CPUS01  
CURRENT APPLICATION NUMBER: US/10/310, 914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 5835  
LENGTH: 82  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-5835

Query Match 8.4%; Score 82; DB 8; Length 82;  
Best Local Similarity 76.8%; Pred. No. 2.5e-09;  
Matches 63; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

QY 265 TCTACACCTGGAGGCTTGGCGACGATGCTTGTCTGAGAGATGAAAAGTCCCAAGTTT 324  
DB 1 UCUCACACCTGGAGGCTTGGCGACGATGCTTGTCTGAGAGATGAAAAGTCCCAAGTUU 60  
QY 325 GCCGCTGCAAGTGAAGTGTGA 346  
DB 61 GCCGCTGCAAGTGAAGTGTGA 82

## RESULT 3

US-10-310-914A-5873  
Sequence 5873, Application US/10310914A  
Publication No. US20060003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shiller, Kiyuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
FILE OF INVENTION: uses thereof  
FILE REFERENCE: 06087, 0200, CPUS01  
CURRENT APPLICATION NUMBER: US/10/310, 914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 5873  
LENGTH: 82  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-5873

Query Match 8.4%; Score 82; DB 8; Length 82;  
Best Local Similarity 76.8%; Pred. No. 2.5e-09;  
Matches 63; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

QY 265 TCTACACCTGGAGGCTTGGCGACGATGCTTGTCTGAGAGATGAAAAGTCCCAAGTTT 324  
DB 1 UCUCACACCTGGAGGCTTGGCGACGATGCTTGTCTGAGAGATGAAAAGTCCCAAGTUU 60  
QY 325 GCCGCTGCAAGTGAAGTGTGA 346  
DB 61 GCCGCTGCAAGTGAAGTGTGA 82

## RESULT 4

US-11-137-465-14  
Sequence 14, Application US/11137465  
Publication No. US20050255558A1  
GENERAL INFORMATION:  
APPLICANT: Agarwal, Pankaj  
APPLICANT: Murdoch, Paul R.  
APPLICANT: Rizvi, Safia, K.  
APPLICANT: Smith, Randall, F.  
APPLICANT: Xiang, Zhaoying  
APPLICANT: Kadnick, Karen  
TITLE OF INVENTION: NOVEL COMPOUNDS  
FILE REFERENCE: GP50018  
CURRENT APPLICATION NUMBER: US/11/137, 465  
CURRENT FILING DATE: 2005-05-25  
PRIOR APPLICATION NUMBER: US/10/239, 663  
PRIOR FILING DATE: 2002-09-24  
PRIOR APPLICATION NUMBER: PCT/US01/09226  
PRIOR FILING DATE: 2001-03-22  
PRIOR APPLICATION NUMBER: 60/192, 158  
PRIOR FILING DATE: 2000-03-24  
PRIOR APPLICATION NUMBER: 60/192, 668  
PRIOR FILING DATE: 2000-03-27  
PRIOR APPLICATION NUMBER: 60/200, 166  
PRIOR FILING DATE: 2000-04-27  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 14  
LENGTH: 1647  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-137-465-14

Query Match 6.8%; Score 67; DB 12; Length 1647;  
Best Local Similarity 63.2%; Pred. No. 1.8e-05;  
Matches 103; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 134 CGCGAGATCTGTCTCCGCCCCCTAGACTAGAGACCCGCGGCCCCCTACTTCCCTTA 193  
DB 1065 CGCGAGATCTGTCTCCGCCCCCTAGACTAGAGACCCGCGGCCCCCTACTTCCCTTA 1124  
QY 194 CTACTAGACAGATGACGACAGAGCTGCGCCAGTCTCTGTACCGGGGCTGCGAGGCGAA 253  
DB 1125 GCGCTACAGCCCGCTGCTGACGAGAGTCCCTCTGTATCCGTGTGCTGCGAGGCGAA 1184  
QY 254 GCGCAACATTTTACACTTGGAGAGGCTTGGAGAGATGCTTG 296

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 9, 2006, 19:49:24 ; Search time 189 Seconds

(without alignments)  
546.318 Million cell updates/sec

Title: US-10-800-057-2

Sequence: 1 MDPARPLGSLILFLTEAA.....KKMPKLRFAFRIRKIRKQF 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A\_Geneseq\_21: \*  
1: geneseqp1980s: \*  
2: geneseqp1980s: \*  
3: geneseqp2000s: \*  
4: geneseqp2001s: \*  
5: geneseqp2002s: \*  
6: geneseqp2003as: \*  
7: geneseqp2003bs: \*  
8: geneseqp2004s: \*  
9: geneseqp2005s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1306	100.0	235	2 AAR74977	AAR74977 Human Kun
2	1306	100.0	235	4 AAB76856	AAB76856 Human Lun
3	1306	100.0	235	5 ABG96429	ABG96429 Human ova
4	1306	100.0	235	5 AAU85511	AAU85511 Clone #19
5	1306	100.0	235	5 ABP68618	ABP68618 Human pan
6	1306	100.0	235	6 ABU03481	ABU03481 Angiogene
7	1306	100.0	235	6 ABUS6599	ABUS6599 Lung canc
8	1306	100.0	235	6 ABUS9483	ABUS9483 Human Lun
9	1306	100.0	235	6 ABUS6385	ABUS6385 Lung canc
10	1306	100.0	235	7 ADH45851	ADH45851 Human Lun
11	1306	100.0	235	7 ADI62727	ADI62727 Human apo
12	1306	100.0	235	7 ADN8706	ADN8706 Cancer/an
13	1306	100.0	235	8 ADL71603	ADL71603 Human Lun
14	1306	100.0	235	8 ADL83255	ADL83255 Human PRO
15	1306	100.0	235	8 ADJ19770	ADJ19770 Human Lun
16	1306	100.0	235	8 ADU06660	ADU06660 Novel bro
17	1306	100.0	235	8 ADZ87320	ADZ87320 Human tis
18	1290	98.8	245	8 ABM83218	ABM83218 Human dia
19	1200	91.9	213	6 AAW61535	AAW61535 Human tis
20	1200	91.9	213	6 ABU07725	ABU07725 Human tis
21	1136.5	87.0	210	4 AAU02970	AAU02970 Angioteins
22	1126.5	86.3	211	4 AAU02969	AAU02969 Angioteins
23	986	75.5	188	4 AAU02979	AAU02979 Angioteins
24	464	35.5	88	6 ABR39435	ABR39435 Human GEN

25	394.5	30.2	291	6 ABR48476	ABr48476 Human Tif
26	393.5	30.1	291	6 ABR48478	ABr48478 Human Tif
27	388	29.7	304	2 AAR67994	AAR67994 Tissue fa
28	388	29.7	304	2 AAR81884	AAR81884 Lipoprote
29	388	29.7	304	2 AAY49557	AAY49557 Human lip
30	388	29.7	304	2 ADY09568	ADY09568 Human tis
31	388	29.7	304	8 ADQ88030	ADQ88030 Human ser
32	388	29.7	304	8 ADL14411	ADL14411 Human NF-
33	388	29.7	304	8 ADU06597	ADU06597 Novel bro
34	388	29.7	304	8 ADU73579	ADU73579 Human tis
35	388	29.7	304	9 ADY36969	ADY36969 Human ser
36	388	29.7	304	9 ADY58286	ADY58286 Human ser
37	387.5	29.7	276	2 AAR92012	AAR92012 TPPI mute
38	387.5	29.7	276	2 AAR92265	AAR92265 TPPI mute
39	387	29.6	304	2 AAR78389	AAR78389 Human lip
40	384.5	29.4	276	2 AAW30311	AAW30311 Recombina
41	384.5	29.4	276	2 AAW61535	AAW61535 Human tis
42	384.5	29.4	276	6 ABU07724	ABU07724 Human tis
43	384.5	29.4	276	7 ADE80824	ADE80824 Human tis
44	384.5	29.4	276	7 ADE80822	ADE80822 Human tis
45	384.5	29.4	276	7 ADI20097	ADI20097 Human TFP

## ALIGNMENTS

RESULT 1	AAR74977	standard; protein, 235 AA.
XX	AA74977;	
AC	21-JUN-1996	(first entry)
XX		
DT	Human Kunitz-type protease-inhibitor TPPI-2.	
XX		
DE	Kunitz-type inhibitor; protease-inhibitor; enzyme-inhibitor;	
KW	anticoagulant; deep vein thrombosis.	
KM		
XX		
OS	Homo sapiens.	
XX		
PN	W09512674-A1.	
XX		
PD	11-MAY-1995.	
XX		
PF	02-NOV-1994; 94MO-US012609.	
XX		
PR	05-NOV-1993; 93US-00147710.	
XX		
PA	(ZYMO) ZYMOGENETICS INC.	
PA	(UNNE-) UNIV NEW MEXICO STATE.	
PI	Sprecher CA, Kistiel W, Foster DC;	
DR	WPI; 1995-193821/25.	
XX	N-FSDB; AAG090469.	
PT	Human Kunitz-type protease inhibitors - used as anticoagulants and in the	
XX	treatment of deep vein thrombosis.	
PS	Claim 2; Page 50; 65pp; English.	
XX		
CC	KTI is used to inhibit blood coagulation in mammals. It is particularly	
CC	used as an anticoagulant and in the treatment of deep vein thrombosis,	
CC	disseminated intravascular coagulations, pulmonary embolism and in the	
CC	prevention of thrombosis following surgery. KTI inhibits Factor-VIIa in	
CC	the absence of Factor-Xa, and thus does not require production of Factor-	
CC	Xa via the intrinsic or extrinsic pathway. This KTI protein shares AA	
CC	sequence homology and overall domain organization with tissue factor	
XX	pathway-inhibitor (TFPI), and has therefore been designated TPPI-2	
XX	Sequence 235 AA;	
XX		

Query Match 100.0%; Score 1306; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 4.5e-114;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGSLILLFLTEALGDAOEPGNNAEICLLPLDYGPCRALIRYYDRYTOS 60  
DB 1 MDPARPLGSLILLFLTEALGDAOEPGNNAEICLLPLDYGPCRALIRYYDRYTOS 60  
QY 61 CRQFLYGCGEGNANFYTWACDCAWRIEKVPKVCRLQVSDQCEGSTEKFFNLSSM 120  
DB 61 CRQFLYGCGEGNANFYTWACDCAWRIEKVPKVCRLQVSDQCEGSTEKFFNLSSM 120  
QY 121 TCEKFPSSGCHNRRIENRPDEATCMGFCAPKKIPSCYSPDEGLCSANVTYYFNPRY 180  
DB 121 TCEKFPSSGCHNRRIENRPDEATCMGFCAPKKIPSCYSPDEGLCSANVTYYFNPRY 180  
QY 181 RTCDAPFTYTCGGNDNNFVSRBDCRACAKALKKKKKMPLRPAIRIRIRKKQF 235  
DB 181 RTCDAPFTYTCGGNDNNFVSRBDCRACAKALKKKKKMPLRPAIRIRIRKKQF 235

## RESULT 2

AAB76856  
ID AAB76856 standard; protein; 235 AA.  
XX AAB76856;

DT 12-APR-2001 (first entry)

DE Human lung tumour protein related protein sequence SEQ ID NO:332.

KM Human; lung cancer; lung tumour; lung tumour protein; gene therapy;  
KW lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine;  
CY cytostatic; antic sense inhibition.

OS Homo sapiens.

PN WO200100828-A2.

PD 04-JAN-2001.

PF 30-JUN-2000; 2000MO-US018061.

PR 30-JUN-1999; 99US-00346492.

PR 15-OCT-1999; 99US-00419356.

PR 17-DEC-1999; 99US-00466867.

PR 30-DEC-1999; 99US-00476300.

PR 06-MAR-2000; 2000US-00519642.

PR 22-MAR-2000; 2000US-00533077.

PR 10-APR-2000; 2000US-00546259.

PR 27-APR-2000; 2000US-00560406.

PR 05-JUN-2000; 2000US-00589184.

(COR-) CORIXA CORP.

PI Wang T, Bangur GS, Lodes MJ, Fanger GR, Vedvick TS, Carter D;  
PI Retter MW, Mannion J;

DR WPI; 2001-071488/08.

PT Lung tumor-associated proteins and the nucleic acids that encode them,  
XX useful for preventing, diagnosing and treating lung cancer.

PS Example 1; Page 260-261; 436BP; English.

CC The present invention describes immunogenic portions of lung tumour-  
CC associated proteins (I) and the nucleic acids (NA) that encode them. (I)  
CC have cytostatic activity and can be used in gene therapy, antisense  
CC inhibition and in vaccines. The NA and the lung tumour-associated  
CC proteins they encode may be used in the prevention, treatment and  
CC diagnosis of diseases associated with their inappropriate expression,  
CC especially lung cancers. For example, the NA may be administered to  
CC treat diseases by rectifying mutations or deletions in a patient's genome

CC that affect the activity of the protein by expressing inactive proteins  
CC or to supplement the patient's own production of (I). Additionally, the  
CC NA may be used to produce the lung-tumour associated protein, according  
CC to standard recombinant DNA methodology. Conversely, antisense NA  
CC molecules may be administered to down regulate protein expression by  
CC binding with the cells own genes and preventing their expression. The NA  
CC and complementary sequences may also be used as DNA probes in diagnostic  
CC assays to detect and quantitate the presence of similar NA sequences in  
CC samples, and hence which patients may be in need of treatment for lung  
CC cancer. The (I) may be used as antigens in the production of antibodies  
CC and in assays to identify modulators (agonists and antagonists) of the  
CC expression and activity of the protein. AAF68083 to AAF68878 and AAB76848  
CC to AAB76878 represent human lung tumour protein related nucleotide and  
CC protein sequences which are used in the exemplification of the present  
XX invention

SO Sequence 235 AA;

Query Match 100.0%; Score 1306; DB 4; Length 235;  
Best Local Similarity 100.0%; Pred. No. 4.5e-114;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGSLILLFLTEALGDAOEPGNNAEICLLPLDYGPCRALIRYYDRYTOS 60  
DB 1 MDPARPLGSLILLFLTEALGDAOEPGNNAEICLLPLDYGPCRALIRYYDRYTOS 60

QY 61 CRQFLYGCGEGNANFYTWACDCAWRIEKVPKVCRLQVSDQCEGSTEKFFNLSSM 120  
DB 61 CRQFLYGCGEGNANFYTWACDCAWRIEKVPKVCRLQVSDQCEGSTEKFFNLSSM 120

QY 121 TCEKFPSSGCHNRRIENRPDEATCMGFCAPKKIPSCYSPDEGLCSANVTYYFNPRY 180  
DB 121 TCEKFPSSGCHNRRIENRPDEATCMGFCAPKKIPSCYSPDEGLCSANVTYYFNPRY 180

QY 181 RTCDAPFTYTCGGNDNNFVSRBDCRACAKALKKKKKMPLRPAIRIRIRKKQF 235  
DB 181 RTCDAPFTYTCGGNDNNFVSRBDCRACAKALKKKKKMPLRPAIRIRIRKKQF 235

## RESULT 3

AABG96429  
ID AABG96429 standard; protein; 235 AA.

AC AABG96429;

DT 11-DEC-2002 (first entry)

DE Human ovarian cancer marker M588.

KW Human; ovarian cancer; marker; cancer; familial history; brain disorder;  
KW central nervous system disorder; bacterial meningitis; viral meningitis;  
KW Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus;  
KW brain herniation; inflammation; encephalitis; testicular disorder;  
KW non-tuberculous granulomatous orchitis; connective tissue disorder;  
KW heart disorder; ischaemic heart disease; atherosclerosis; neoplasia;  
KW histological type; carcinogenic; ovarian cancer marker.

OS Homo sapiens.

PN WO200271928-A2.

PD 19-SEP-2002.

PF 14-MAR-2002; 2002MO-US007826.

PR 14-MAR-2001; 2001US-0276025P.

PR 14-MAR-2001; 2001US-0276025P.

PR 10-AUG-2001; 2001US-0311732P.

PR 19-SEP-2001; 2001US-0323580P.

PR 26-SEP-2001; 2001US-0324967P.

PR 26-SEP-2001; 2001US-0325102P.

PR 26-SEP-2001; 2001US-0325149P.



PA (MILL-) MILLENNIUM PHARM INC.  
XX  
XX Monahan JE, Gamaavarapu M, Hoersch S, Kamathar S, Kovatis SG,  
PI Meyers RE, Morrissey MP, Olandt PJ, Sen A, Vleby PO, Mills GB,  
PI Best RC, Lu K, Schmandt RE, Zhao X, Glatt K;  
XX  
XX WPI: 2002-72377/78.  
DR N-P8DB; AB876528.  
XX  
XX Assessing whether a patient is afflicted with ovarian cancer, useful in  
PT assessing the stage or progression of the disease, comprises comparing  
PT the expression level of a cancer marker in a sample from a patient and  
PT from a non cancer patient.  
XX  
XX Disclosure; Page 437-438; 481pp; English.  
XX  
XX The present invention relates to a new method for assessing whether a  
CC patient is afflicted with ovarian cancer. The method involves comparing  
CC the expression level of a marker in a patient sample and the normal level  
CC of expression of the marker in a control non-ovarian cancer sample, where  
CC the marker is selected from 363 cancer markers described in the  
CC specification. The method of the invention is useful in diagnosing or  
CC characterizing cancer, in detecting the presence of cancer as early as  
CC possible, and the recurrence of ovarian cancer. The method may also be of  
CC particular use with patients having an enhanced risk of developing  
CC ovarian cancer (e.g. patients having a familial history of ovarian  
CC cancer). The cancer markers may be used in the management and treatment  
CC of e.g. brain and central nervous system disorders (e.g. bacterial and  
CC viral meningitis, Alzheimer's disease or Parkinson's disease), brain  
CC disorders (e.g. cerebral oedema, hydrocephalus or brain herniations),  
CC inflammations (e.g. bacterial or viral meningitis or encephalitis),  
CC testicular disorders (e.g. nonbacterial granulomatous orchitis),  
CC connective tissue disorders, or heart disorders (e.g. ischemic heart  
CC disease or atherosclerosis). The compositions and methods may also be  
CC used in assessing the histological type of neoplasm associated with  
CC ovarian cancer, monitoring the progression of ovarian cancer, determining  
CC whether ovarian cancer has metastasized or is likely to metastasize,  
CC selecting a composition for inhibiting ovarian cancer, assessing the  
CC ovarian carcinogenic potential of a compound, or inhibiting ovarian  
CC cancer or at risk of developing ovarian cancer. The present amino acid  
CC sequence represents one of the ovarian cancer markers described in the  
CC invention  
XX  
XX  
XX Sequence 235 AA;  
SQ  
Query Match 100.0%; Score 1306; DB 5; Length 235;  
Best Local Similarity 100.0%; Pred. No. 4.5e-114;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDPAPRLGISILLPTTEALGDPAOEPYNNNAETCLPLDVGPCALILRYDYDTOS 60  
DB 1 MDPAPRLGISILLPTTEALGDPAOEPYNNNAETCLPLDVGPCALILRYDYDTOS 60  
QY 61 CROPLVGGCEGNANNTYWEACDCAWRIEKPVKYCRLOVSVDQEGSTETKFFNLSSM 120  
DB 61 CROPLVGGCEGNANNTYWEACDCAWRIEKPVKYCRLOVSVDQEGSTETKFFNLSSM 120  
QY 121 TCEKFPSSGGCHNRRIENRPDEATCMGFCAPKKIISFCYSPXDBGLCSANVTRYENPRY 180  
DB 121 TCEKFPSSGGCHNRRIENRPDEATCMGFCAPKKIISFCYSPXDBGLCSANVTRYENPRY 180  
QY 181 RTCDATFTYTCGGGNDNNFVSRBCKRAKAKLKKKKMPKLRPASIRIKRKQF 235  
DB 181 RTCDATFTYTCGGGNDNNFVSRBCKRAKAKLKKKKMPKLRPASIRIKRKQF 235  
RESULT 4  
AA085511  
ID AA085511 standard; protein; 235 AA.  
XX  
XX AA085511,  
AC  
XX  
DT 21-MAY-2002 (first entry)

XX  
XX Clone #19117 of lung tumour protein.  
DE  
XX  
XX Lung tumour; cancer; T cell; immune response stimulator; cytostatic.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200204514-A2.  
PN  
XX  
XX 17-JAN-2002.  
PD  
XX  
XX 10-JUL-2001; 2001WO-US022058.  
PF  
XX  
XX 11-JUL-2000; 2000US-00614124.  
PR 29-AUG-2000; 2000US-00651553.  
PR 08-SEP-2000; 2000US-00658824.  
PR 26-SEP-2000; 2000US-00671325.  
PR 06-OCT-2000; 2000US-00677419.  
PR 30-OCT-2000; 2000US-00702705.  
PR 13-DEC-2000; 2000US-00736457.  
PR 03-MAY-2001; 2001US-00849626.  
XX  
XX (CORI-) CORIXA CORP.  
PA  
XX  
XX Wang T, Matanabe Y, Henderson RA, Johnson JC, Retter MM;  
PI Marnerakis M, Carter D, Fanger GR, Vedgwick TS, Bangur CS, Menabdi A,  
PI Wang A, Fanger N, Switzer A, McNeill PD, Clapper JD;  
XX  
XX WPI: 2002-164634/21.  
DR N-P8DB; ABK38057.  
XX  
XX Novel polynucleotide encoding a lung tumor polypeptide useful for  
PT stimulating and/or expanding T cells specific for a tumor protein.  
PT  
XX  
XX Example 1; SEQ ID NO 332; 223pp; English.  
PS  
XX  
XX The invention describes an isolated polynucleotide and polypeptide useful  
CC for stimulating and/or expanding T cells specific for a tumor protein  
CC for determining the presence of a cancer in a patient. A composition  
CC containing the polynucleotide and/or polypeptide is useful for treating a  
CC lung cancer in a patient. The polypeptide is useful for removing tumour  
CC cells from a biological sample. The polynucleotide is also useful as  
CC probe or primer to detect the level of mRNA encoding a tumour protein.  
CC This is the amino acid sequence of a lung tumour associated protein.  
CC described in the method of the invention. Note: The sequence data for  
CC this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX  
XX Sequence 235 AA;  
SQ  
Query Match 100.0%; Score 1306; DB 5; Length 235;  
Best Local Similarity 100.0%; Pred. No. 4.5e-114;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDPAPRLGISILLPTTEALGDPAOEPYNNNAETCLPLDVGPCALILRYDYDTOS 60  
DB 1 MDPAPRLGISILLPTTEALGDPAOEPYNNNAETCLPLDVGPCALILRYDYDTOS 60  
QY 61 CROPLVGGCEGNANNTYWEACDCAWRIEKPVKYCRLOVSVDQEGSTETKFFNLSSM 120  
DB 61 CROPLVGGCEGNANNTYWEACDCAWRIEKPVKYCRLOVSVDQEGSTETKFFNLSSM 120  
QY 121 TCEKFPSSGGCHNRRIENRPDEATCMGFCAPKKIISFCYSPXDBGLCSANVTRYENPRY 180  
DB 121 TCEKFPSSGGCHNRRIENRPDEATCMGFCAPKKIISFCYSPXDBGLCSANVTRYENPRY 180  
QY 181 RTCDATFTYTCGGGNDNNFVSRBCKRAKAKLKKKKMPKLRPASIRIKRKQF 235  
DB 181 RTCDATFTYTCGGGNDNNFVSRBCKRAKAKLKKKKMPKLRPASIRIKRKQF 235  
RESULT 5

ABP68618  
ID ABP68618 standard; protein; 235 AA.  
XX  
AC ABP68618;  
XX  
DT 14-JAN-2003 (first entry)  
XX  
DE Human pancreatic cancer expressed protein SEQ ID NO 167.  
XX  
KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;  
XX  
KW cytostatic; tumour.  
XX  
OS Homo sapiens.  
XX  
PN WO200260317-A2.  
XX  
PD 08-AUG-2002.  
XX  
PP 30-JAN-2002; 2002WO-US002781.  
XX  
PR 30-JAN-2001; 2001US-0265305P.  
XX  
PR 31-JAN-2001; 2001US-0265682P.  
XX  
PR 09-FEB-2001; 2001US-0267568P.  
XX  
PR 21-MAR-2001; 2001US-0278651P.  
XX  
PR 28-APR-2001; 2001US-0287112P.  
XX  
PR 16-MAY-2001; 2001US-0291631P.  
XX  
PR 12-JUL-2001; 2001US-0305484P.  
XX  
PR 20-AUG-2001; 2001US-0313999P.  
XX  
PR 27-NOV-2001; 2001US-0333626P.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Benson DR, Kalos MD, Iodes MJ, Persing DH, Hepler WT, Jiang Y;  
XX  
DR WPI; 2002-627435/67.  
XX  
DR N-PSDB; ABV94764.  
XX  
PT New isolated polynucleotide and pancreatic tumor polypeptides, useful for  
XX  
PT diagnosing, preventing and/or treating cancer, particularly pancreatic  
XX  
PT cancer.  
XX  
PS Claim 2; SEQ ID NO 167; 300pp + Sequence Listing; English.  
XX  
XX  
CC The invention relates to an isolated polynucleotide (1) comprising: (a)  
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)  
CC complements of (a); (c) sequences consisting of at least 20 contiguous  
CC residues of (a); (d) sequences that hybridize to (a), under moderately  
CC stringent conditions; (e) sequences having at least 75% or 90% identity  
CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68536-  
CC ABP68637) encoded by (1) and oligonucleotide can be used to detect cancer  
CC in a patient and compositions comprising polypeptides, polynucleotides,  
CC antibodies, fusion proteins, T cell populations and antigen presenting  
CC cells expressing the polypeptide are useful in treating pancreatic cancer  
CC and stimulating an immune response. The polynucleotide can be used as  
CC probes or primers for nucleic acid hybridization, in the design and  
CC preparation of ribozyme molecules for inhibiting expression of the tumour  
CC polypeptides and proteins in the tumour cells, in vaccines and for gene  
CC therapy. Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX  
SQ Sequence 235 AA;  
XX

Query Match 100.0%; Score 1306; DB 5; Length 235;  
Best Local Similarity 100.0%; Pred. No. 4.5e-114;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MDPAPPLGSLILLPTETALGDAAQEPYNNACILCLPLDYGPCRALLRYYDRYQS 60  
1 MDPAPPLGSLILLPTETALGDAAQEPYNNACILCLPLDYGPCRALLRYYDRYQS 60  
1 MDPAPPLGSLILLPTETALGDAAQEPYNNACILCLPLDYGPCRALLRYYDRYQS 60  
61 CROFLYGGCGEANNPFTWEACDDACWRLEKVPKVCRLQVSDDCGEGSTKKYFNLSSM 120  
|||||

DB 61 CROFLYGGCGEANNPFTWEACDDACWRLEKVPKVCRLQVSDDCGEGSTKKYFNLSSM 120  
QY 121 TCEKFFSGGCHNRRIENRPPDQATGFCAPKKIFSPFCYSPROEGLCSANVTRYFNPRY 180  
DB 121 TCEKFFSGGCHNRRIENRPPDQATGFCAPKKIFSPFCYSPROEGLCSANVTRYFNPRY 180  
QY 181 RTCDAPFTYTGCGGNDNNFVSRDCCRACAKALKKKKMKLPASIRIRKRRKQF 235  
DB 181 RTCDAPFTYTGCGGNDNNFVSRDCCRACAKALKKKKMKLPASIRIRKRRKQF 235  
RESULT 6  
ABU03481  
ID ABU03481 standard; protein; 235 AA.  
XX  
AC ABU03481;  
XX  
DT 21-JAN-2003 (first entry)  
XX  
DE Angiogenesis-associated human protein sequence #26.  
XX  
KW Human; angiogenesis-associated transcript; angiogenesis;  
XX  
KW angiogenesis-associated disease; cancer; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN WO200279492-A2.  
XX  
PD 10-OCT-2002.  
XX  
PP 14-FEB-2002; 2002WO-US004915.  
XX  
PR 14-FEB-2001; 2001US-00784356.  
XX  
PR 22-FEB-2001; 2001US-00791390.  
XX  
PR 19-APR-2001; 2001US-0286475P.  
XX  
PR 03-AUG-2001; 2001US-0310025P.  
XX  
PR 13-NOV-2001; 2001US-0350666P.  
XX  
PR 29-NOV-2001; 2001US-0334244P.  
XX  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
XX  
PI Murray R, Glynn R, Watson SR, Aziz N;  
XX  
DR WPI; 2003-040681/03.  
XX  
DR N-PSDB; ABX08764.  
XX  
PT Detecting angiogenesis-associated transcript in a cell for diagnosing and  
XX  
PT treating cancer by contacting a sample with a polynucleotide that  
XX  
PT exhibits changes in expression level as a function of time in tissue  
XX  
PT undergoing angiogenesis.  
XX  
PS Example 2; Page 205; 291pp; English.  
XX  
XX  
CC The present invention relates to methods and compositions for detecting  
CC an angiogenesis-associated transcript in a cell in a patient. The method  
CC involves contacting a biological sample from the patient with a  
CC polynucleotide that selectively hybridizes to a sequence at least 80%  
CC identical to any of the angiogenesis-associated human polynucleotide  
CC sequences given in the specification. These angiogenesis-associated  
CC polynucleotide sequences comprise genes that exhibit changes in  
CC expression levels as a function of time in tissue undergoing  
CC angiogenesis. The method and the polynucleotide sequences of the  
CC invention are useful for diagnosing and treating angiogenesis and  
CC angiogenesis-associated diseases e.g. cancer. The polynucleotide  
CC sequences are also useful in the gene therapy of such disorders. The  
CC angiogenesis-associated proteins encoded by the polynucleotide sequences  
CC are useful as a vaccine for therapeutic and prophylactic immunization.  
XX  
XX  
SQ Sequence 235 AA;  
XX

Query Match 100.0%; Score 1306; DB 6; Length 235;  
Best Local Similarity 100.0%; Pred. No. 4.5e-114;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGISLTLPLTEALGDAAQEPGNNAEICLPLDYGPCRALLRYYRYTQS 60  
 CC lung cancer; or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences CC ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the CC invention

Db 61 CRQPLVGGCGEGNANFYTWACDDACWRIEKVPKVCRLQVSDVDDCGESTETKYPFLISM 120  
 CC for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences CC ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the CC invention

QY 121 TCEKFPSSGGCHNRRIENRPPDEATCMGFCAPKKIIPSCYSPDEGLCSANVTYYFNPRY 180  
 CC lung cancer-associated polypeptide #192.

Db 121 TCEKFPSSGGCHNRRIENRPPDEATCMGFCAPKKIIPSCYSPDEGLCSANVTYYFNPRY 180

QY 181 RTCDAPFTYTGCGGNNNFVSRDCCRACAKALKKKKKMPKLPASRIRIRKKOP 235  
 CC lung cancer-associated polypeptide #192.

Db 181 RTCDAPFTYTGCGGNNNFVSRDCCRACAKALKKKKKMPKLPASRIRIRKKOP 235

RESULT 7  
 ID ABUS6599 standard; protein, 235 AA.  
 AC ABUS6599;  
 DT 02-APR-2003 (first entry)  
 DE Lung cancer-associated polypeptide #192.  
 XX Lung cancer-associated polypeptide; cytostatic; emphysema; antiinflammatory; antineoplastic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lesion; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.  
 XX Undifferentiated.  
 OS WO200286443-A2.  
 PN 31-OCT-2002.  
 PD 18-APR-2002; 2002WO-US012476.  
 PF 18-APR-2001; 2001US-02984770P.  
 PR 10-MAY-2001; 2001US-0290492P.  
 PR 09-NOV-2001; 2001US-0339245P.  
 PR 13-NOV-2001; 2001US-0350666P.  
 PR 29-NOV-2001; 2001US-0334370P.  
 PR 12-APR-2002; 2002US-0372246P.  
 XX (EOSB-) EOS BIOTECHNOLOGY INC.  
 PA Aziz N, Murray R;  
 PI WPI; 2003-093161/08.  
 DR N-PSDB; ABX76328.  
 XX Claim 27; Page 333; 453p; English.

The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by

CC administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences CC ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the CC invention

SQ Sequence 235 AA;

Query Match 100.0%; Score 1306; DB 6; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-114;  
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGISLTLPLTEALGDAAQEPGNNAEICLPLDYGPCRALLRYYRYTQS 60  
 Db 1 MDPARPLGISLTLPLTEALGDAAQEPGNNAEICLPLDYGPCRALLRYYRYTQS 60

QY 61 CRQPLVGGCGEGNANFYTWACDDACWRIEKVPKVCRLQVSDVDDCGESTETKYPFLISM 120  
 Db 61 CRQPLVGGCGEGNANFYTWACDDACWRIEKVPKVCRLQVSDVDDCGESTETKYPFLISM 120

QY 121 TCEKFPSSGGCHNRRIENRPPDEATCMGFCAPKKIIPSCYSPDEGLCSANVTYYFNPRY 180  
 Db 121 TCEKFPSSGGCHNRRIENRPPDEATCMGFCAPKKIIPSCYSPDEGLCSANVTYYFNPRY 180

QY 181 RTCDAPFTYTGCGGNNNFVSRDCCRACAKALKKKKKMPKLPASRIRIRKKOP 235  
 Db 181 RTCDAPFTYTGCGGNNNFVSRDCCRACAKALKKKKKMPKLPASRIRIRKKOP 235

RESULT 8  
 ID ABUS6483 standard; protein, 235 AA.  
 AC ABUS6483;  
 DT 05-JUN-2003 (first entry)  
 DE Human lung cancer associated cDNA #19117protein.  
 XX Human; lung cancer; lung tumour; cytostatic; vaccine; T cell expansion; CD4; CD8.  
 OS Homo sapiens.  
 XX US2002197669-A1.  
 PN 26-DEC-2002.  
 PD 03-MAY-2001; 2001US-00849626.  
 PF 13-DEC-2000; 2000US-00736457.  
 PR (BANG/) BANGUR C S.  
 PA (FANG/) FANGER G R.  
 PA (WANG/) WANG A.  
 PA (WANG/) WANG T.  
 PA (SWIT/) SWITZER A P.  
 PA (MCNE/) MCNEILL P D.  
 PA (CLAP/) CLAPPER J D.  
 XX Bangur CS, Fanger GR, Wang A, Wang T, Switzer AP, Mcneill PD;  
 PI Clapper JD;  
 XX WPI; 2003-352750/33.  
 DR N-PSDB; ACA10386.  
 XX Novel lung cancer polynucleotide encoding lung cancer protein, useful for detecting the presence of lung cancer in a patient, and in pharmaceutical



DB 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKMKPLRFPASIRIRKIRKQF 235

RESULT 10

ID ADH45851 standard; protein; 235 AA.

AC ADH45851;

XX

XX

XX 25-MAR-2004 (first entry)

DT

XX Human lung tumour clone protein, SEQ ID NO 332.

DE

XX Human lung tumour; cytostatic; immunostimulant; vaccine; gene therapy;

KW human; clone.

XX

XX Homo sapiens.

OS

XX MO2003037267-A2.

PN

XX 08-MAY-2003.

PD

XX 28-OCT-2003; 2002WO-US034777.

PF

XX 29-OCT-2001; 2001US-00017754.

PR

XX 28-MAR-2002; 2002US-00113872.

PA

XX (CORI-) CORIXA CORP.

XX Henderson RA, Wang T, Watanabe Y, Kalos MD, Sleath PR;

PI Johnson JC, Retter MW, Durham M, Carter D, Fanger GR, Vedvick TS;

PI Bangur CS, Mcnabb A;

XX WPI; 2003-468346/44.

DR

XX New polypeptides and encoding polynucleotides, useful for diagnosing,

PT preventing and/or treating lung cancer.

XX

XX Example 1; SEQ ID NO 332; 258bp; English.

PS

XX The invention relates to novel compositions and methods for the therapy

XX and diagnosis of cancer, particularly lung cancer. The compositions

CC comprise one or more lung tumour polypeptides, immunogenic portions

CC thereof, polynucleotides that encode such polypeptides, antigen presenting

CC cells that express such polypeptides, and T cells that are specific for

CC cells expressing such polypeptides. The novel compositions have

CC cytostatic and immunostimulant activity. The lung tumour antigens can be

CC used in the creation of a vaccine. The polynucleotides that encode the

CC lung tumour polypeptides can be used in gene therapy to help in the

CC treatment of lung tumours. This sequence represents a human lung tumour

CC clone polypeptide of the invention. This sequence was not shown in the

CC specification. It has been taken from a World Intellectual Property

CC Organization CD ROM supplied with the specification.

XX

XX Sequence 235 AA;

SO

Query Match 100.0%; Score 1306; DB 7; Length 235;

Best/Local Similarity 100.0%; Pred. No. 4,5e-114;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDBARPLGSLILFLTBALGDAOBPTGNMNEICLPLDVGPCRALIRYYDRYTOS 60

DB 1 MDBARPLGSLILFLTBALGDAOBPTGNMNEICLPLDVGPCRALIRYYDRYTOS 60

QY 61 CRQFLYGGCGEGNANNFTWEACDCAWRLEKVPKGLQVSVDOEGSGSTKFFNLSSM 120

DB 61 CRQFLYGGCGEGNANNFTWEACDCAWRLEKVPKGLQVSVDOEGSGSTKFFNLSSM 120

QY 121 TCSEKPSGGGCHRRRIENRFPDEATCMGFCAPKCI PSFCISPKDBGLCSANVTYTRNPKY 180

DB 121 TCSEKPSGGGCHRRRIENRFPDEATCMGFCAPKCI PSFCISPKDBGLCSANVTYTRNPKY 180

QY 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKMKPLRFPASIRIRKIRKQF 235

DB 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKMKPLRFPASIRIRKIRKQF 235

RESULT 11

ID ADI62727 standard; protein; 235 AA.

AC ADI62727;

XX

XX

XX 08-SEP-2005 (revised)

DT

XX 22-APR-2004 (first entry)

DE

XX Human apoptosis-associated protein SEQ ID 170.

DE

XX apoptosis; cell death; cytostatic; neuroprotective; immunosuppressive;

KW antiinflammatory; antiarthritic; dermatological; antiparkinsonian;

KW hepatotropic; vitruic; neurotic; anticonvulsant; antiparkinsonian;

KW vasotrophic; cerebroprotective; antialcoholic; gene therapy; tumour;

KW autoimmune disease; degenerative disease; viral infection; leukaemia;

KW carcinoma; sarcoma; multiple sclerosis; rheumatoid arthritis; diabetes;

KW lupus; hepatitis; influenza viruses; Alzheimer's disease;

KW Huntington's disease; Parkinson's disease; reperfusion injury; stroke;

KW alcoholic liver disease; human.

XX

XX Homo sapiens.

OS

XX MO2003058021-A2.

PN

XX 17-JUL-2003.

PD

XX 13-JAN-2003; 2003WO-EP000270.

PF

XX 11-JAN-2002; 2002DB-01000856.

PR

XX (XANT-) XANTOS BIOMEDICINE AG.

PA

XX Koenig-Hoffman K, Kazinski M, Schaefer R, Keeper B;

PI WPI; 2003-542134/51.

PI N-PSDB; AEA79099.

DR

XX New nucleic acids involved in apoptosis, useful for diagnosis and

PT treatment of e.g. tumors and degenerative disease, also related proteins,

PT antibodies and modulators.

XX

XX Claim 1a; SEQ ID NO 170; 517bp; German.

PS

XX This invention describes novel nucleic acid molecules that are associated

XX with apoptosis and encode a polypeptide and are derived from a normalised

CC gene library (embryonic or liver) or clone collections, and the extent of

CC apoptosis measured by cell death detection assay or the CPG assay

CC (measuring loss of membrane integrity). The products of the invention

CC have cytostatic, neuroprotective, immunosuppressive, antiinflammatory,

CC antiarthritic, dermatological, antiparkinsonian, hepatotropic, vitruic,

CC neurotropic, anticonvulsant, antiparkinsonian, vasotrophic,

CC cerebroprotective and antialcoholic activity and can be used for gene

CC therapy. The polynucleotides also related vectors, hosts (or their

CC extracts), encoded polypeptide (or their receptors) and/or agents that

CC inhibit their activity (including antisense sequences) are used for

CC treatment or prevention of tumours, autoimmune or degenerative diseases

CC and viral infections, specifically leukaemia, carcinoma, sarcoma,

CC multiple sclerosis, influenza viruses, Alzheimer's, Huntington's or

CC Parkinson's diseases, reperfusion injury, stroke and alcoholic liver

CC disease. Detection of the polynucleotides and derived polypeptides can

CC also be used for diagnosis of these diseases. This sequence represents an

CC apoptosis-associated protein described in the invention.

CC

CC Revised record issued on 08-SEP-2005 : Revision to cross-reference field

XX

XX Sequence 235 AA;

SO



PA (BANG/) BANGUR C S.  
XX  
XX Wang T, Bangur CS;  
XX WPI; 2004-059187/06.  
DR N-PSDB; AD872120.  
XX  
XX Compositions and methods for the therapy and diagnosis of lung cancer  
PT based on the detection of a lung tumor polypeptide or immunogenic portion  
PT of this lung tumor protein.  
XX  
XX Claim 52; SEQ ID NO 332; 38pp; English.  
XX  
XX The invention relates to a polypeptide comprising at least an immunogenic  
CC portion of a lung tumor protein or variant. The invention is useful for  
CC inhibiting the development of a cancer, particularly lung cancer, in a  
CC patient by administering to a patient an effective amount of a  
CC polypeptide, an effective amount of the polynucleotide, an effective  
CC amount of an antibody or antigen-binding fragment an antigen-presenting  
CC cell that expresses a polypeptide where the antigen-presenting cell is a  
CC dendritic cell, a biological sample treated by a method of the invention  
CC or an isolated T cell population prepared by a method of the invention.  
CC The pharmaceutical compositions and vaccines of the invention are also  
CC used for inhibiting the development of cancer. Methods are also provided  
CC for diagnosing cancer and also monitoring the progression of cancer.  
CC Current therapies of cancer are based on the combination of chemotherapy  
CC or surgery or radiation which prove to be inadequate in many patients.  
CC This invention provides effective vaccines and compositions which may be  
CC used in therapy. The compositions also provide early diagnostic  
CC procedures. The present sequence represents the amino acid sequence of a  
CC human lung tumour protein.  
XX  
XX Sequence 235 AA;  
SQ  
Query Match 100.0%; Score 1306; DB 8; Length 235;  
Best Local Similarity 100.0%; Pred. No. 4.5e-114;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDPAPPLGSLILLFLTEALGDAAOEPGNNALICLLPLDYGPCRALILRYRYRTYS 60  
DB 1 MDPAPPLGSLILLFLTEALGDAAOEPGNNALICLLPLDYGPCRALILRYRYRTYS 60  
QY 61 CROPFLYGGCGEGNANFYTWBACDDACMRIBKVPKVCRLQVSDQCEGSTEKTFPNLSM 120  
DB 61 CROPFLYGGCGEGNANFYTWBACDDACMRIBKVPKVCRLQVSDQCEGSTEKTFPNLSM 120  
QY 121 TCEKFFSGGCHNRRIENRPPDEATCMGFCAPKCIIPSCYSPDEGLCSANVTTRYFNPRY 180  
DB 121 TCEKFFSGGCHNRRIENRPPDEATCMGFCAPKCIIPSCYSPDEGLCSANVTTRYFNPRY 180  
QY 181 RTCDAPFTTGGCGDNPNFVSREDCKRACAKALKKKKKMPKLRPASIRIKIRKKOP 235  
DB 181 RTCDAPFTTGGCGDNPNFVSREDCKRACAKALKKKKKMPKLRPASIRIKIRKKOP 235  
RESULT 14  
ADL83255 standard; protein; 235 AA.  
ID ADL83255  
AC ADL83255;  
XX  
XX 17-JUN-2004 (first entry)  
XX  
XX Human PRO35972, SEQ ID 457.  
XX  
XX Immunosuppressive; Cytostatic; Antiarthritic; Antipneumatic; Antianemic;  
XX Antiallergic; Muscular; Neuroprotective; Nephrotoxic; Antiinflammatory;  
XX Gene Therapy; PRO; B cell related disorder; cancer;  
XX Immune-mediated inflammatory disease; human.  
XX  
XX Homo sapiens.  
XX  
XX WO2004024097-A2.  
PN

XX  
XX 25-MAR-2004.  
XX  
XX 15-SEP-2003; 2003WO-US029097.  
XX  
XX 16-SEP-2002; 2002US-0411392P.  
XX  
XX (GERTH ) GENENTECH INC.  
XX  
XX Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;  
XX Wu TD;  
XX  
XX WPI; 2004-329389/30.  
DR N-PSDB; ADL83254.  
XX  
XX New PRO polypeptide, useful for diagnosing and treating a B cell related  
PT disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune  
PT mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.  
XX  
XX Claim 10; Fig 457; 695pp; English.  
XX  
XX The present invention relates to PRO proteins and their coding sequences.  
CC The PRO proteins are useful for diagnosing and treating a B cell related  
CC disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide  
CC antigen unresponsiveness, selective IgA deficiency, selective IgM  
CC deficiency, selective deficiency of IgG subclasses, immunodeficiency with  
CC hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's  
CC lymphoma, intermediate lymphoma, follicular lymphoma, type II  
CC hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic  
CC anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or  
CC ankylosing spondylitis. The PRO proteins are also useful for preparing a  
CC medicament for treating a condition that is responsive to the PRO  
CC protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO  
CC coding sequences are useful as hybridization probes in chromosome and  
CC gene mapping, in preparing PRO proteins, or in generating transgenic  
CC animals or knockout animals, which in turn are useful in the development  
CC and screening of therapeutically useful reagents.  
XX  
XX Sequence 235 AA;  
SQ  
Query Match 100.0%; Score 1306; DB 8; Length 235;  
Best Local Similarity 100.0%; Pred. No. 4.5e-114;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDPAPPLGSLILLFLTEALGDAAOEPGNNALICLLPLDYGPCRALILRYRYRTYS 60  
DB 1 MDPAPPLGSLILLFLTEALGDAAOEPGNNALICLLPLDYGPCRALILRYRYRTYS 60  
QY 61 CROPFLYGGCGEGNANFYTWBACDDACMRIBKVPKVCRLQVSDQCEGSTEKTFPNLSM 120  
DB 61 CROPFLYGGCGEGNANFYTWBACDDACMRIBKVPKVCRLQVSDQCEGSTEKTFPNLSM 120  
QY 121 TCEKFFSGGCHNRRIENRPPDEATCMGFCAPKCIIPSCYSPDEGLCSANVTTRYFNPRY 180  
DB 121 TCEKFFSGGCHNRRIENRPPDEATCMGFCAPKCIIPSCYSPDEGLCSANVTTRYFNPRY 180  
QY 181 RTCDAPFTTGGCGDNPNFVSREDCKRACAKALKKKKKMPKLRPASIRIKIRKKOP 235  
DB 181 RTCDAPFTTGGCGDNPNFVSREDCKRACAKALKKKKKMPKLRPASIRIKIRKKOP 235  
RESULT 15  
ADL19770 standard; protein; 235 AA.  
ID ADL19770  
AC ADL19770;  
XX  
XX 04-NOV-2004 (first entry)  
XX  
XX Human lung cancer-related protein - SEQ ID 332.  
XX  
XX Lung tumour; cytostatic; lung cancer; human.  
XX  
XX

OS Homo sapiens.  
XX US2003211510-A1.  
XX 13-NOV-2003.  
XX 28-OCT-2002; 2002US-00283017.  
XX 30-JUN-1999; 99US-00346492.  
XX 15-OCT-1999; 99US-00419356.  
XX 17-DEC-1999; 99US-00466867.  
XX 30-DEC-1999; 99US-00476300.  
XX 06-MAR-2000; 2000US-00519642.  
XX 22-MAR-2000; 2000US-00533077.  
XX 10-APR-2000; 2000US-00546259.  
XX 27-APR-2000; 2000US-00560406.  
XX 05-JUN-2000; 2000US-00589184.  
XX 11-JUL-2000; 2000US-00614124.  
XX 29-AUG-2000; 2000US-00651563.  
XX 08-SEP-2000; 2000US-00658824.  
XX 26-SEP-2000; 2000US-00671325.  
XX 06-OCT-2000; 2000US-00677419.  
XX 30-OCT-2000; 2000US-00702705.  
XX 13-DEC-2000; 2000US-00736457.  
XX 03-MAY-2001; 2001US-00849626.  
XX 10-JUL-2001; 2001US-00902941.  
XX 29-OCT-2001; 2001US-00017754.  
XX 28-MAR-2002; 2002US-00113872.  
XX (CORI-) CORIXA CORP.  
XX Henderson RA, Wang T, Watanabe Y, Kalos MD, Sleath PR,  
XX Johnson JC, Rector WM, Durham M, Carter D, Fanger GR, Vedvick TS,  
XX Bangur CS, McNabb A;  
XX MPI: 2004-167010/16.  
XX N-PSDB; ADI19502.  
XX Novel polynucleotide encoding lung tumor polypeptides, useful for  
XX diagnosing, preventing and treating cancer e.g. lung cancer.  
XX Example 1; SEQ ID NO 332; 99pp; English.  
XX The invention relates to a novel isolated polynucleotide comprising a  
XX sequence chosen from any one of 40 lung tumor polypeptides or its  
XX complements, fragments or degenerate variants. The method of the  
XX invention has cytostatic applications and may be useful for detecting and  
XX treating lung cancer in a patient, as well as for inhibiting the  
XX development of lung cancer in a patient via incubating CD4+ and/or CD8+ T  
XX cells isolated from a patient with at least one component chosen from a  
XX polypeptide, polynucleotide or antigen presenting cell (APC) of the  
XX invention and administering an effective amount of the proliferated T  
XX cells to the patient. The current sequence is that of the human lung  
XX cancer-related protein of the invention. The current sequence is not  
XX shown in the specification per se but is available on the USPTO web-site  
XX http://seqdata.uspto.gov/sequence.html?docid=20030211510.  
XX Sequence 235 AA;  
SQ

Query Match 100.0%; Score 1306; DB 9; Length 235;  
Best Local Similarity 100.0%; Pred. No. 4.5e-114; Indels 0; Gaps 0;  
Matches 235; Conservative 0; Mismatches 0;  
QY 1 MDPARPLGISILLPLTEALGDAAGPTGNNAICILPLDYGPCRALILRYDYDTQS 60  
DB 1 MDPARPLGISILLPLTEALGDAAGPTGNNAICILPLDYGPCRALILRYDYDTQS 60  
QY 61 CRQFLYGGCEGNANFYTWACDCAWRIEKVPKVCRLQVSVDDQCEGSTERYFPNLSSM 120  
DB 61 CRQFLYGGCEGNANFYTWACDCAWRIEKVPKVCRLQVSVDDQCEGSTERYFPNLSSM 120  
QY 121 TCEKPFSGGCHRNRIENRPDEATCMGFCAPIKIPSFCTYSPRDEGLCSANTVTRYFNPXY 180  
DB 121 TCEKPFSGGCHRNRIENRPDEATCMGFCAPIKIPSFCTYSPRDEGLCSANTVTRYFNPXY 180

DB 121 TCEKPFSGGCHRNRIENRPDEATCMGFCAPIKIPSFCTYSPRDEGLCSANTVTRYFNPXY 180  
QY 181 RTCDATFTYTGCGGNDNNFVSRBDCRACAKLKKKKKPKLRFASIRIKRKQF 235  
DB 181 RTCDATFTYTGCGGNDNNFVSRBDCRACAKLKKKKKPKLRFASIRIKRKQF 235

Search completed: March 9, 2006, 19:52:52  
Job time : 192 secs



DB 1185 CGGCAACAACCTTCACAGCCGGAGAGCTGCGAGGATGCTGCTC 1227

RESULT 5  
US-10-821-234-688

/ Sequence 688, Application US/10821234  
/ Publication No. US2005025511A1

GENERAL INFORMATION:

/ APPLICANT: Labat, Ivan  
/ APPLICANT: Stache-Crain, Birgit  
/ APPLICANT: Andarmeni, Susan  
/ APPLICANT: Tang, Y. Tom  
/ TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
/ FILE REFERENCE: 821A

/ CURRENT APPLICATION NUMBER: US/10/821,234

/ PRIOR FILING DATE: 2004-04-07

/ PRIOR APPLICATION NUMBER: US 60/462,047

/ PRIOR FILING DATE: 2003-04-07

/ NUMBER OF SEQ ID NOS: 1704

/ SOFTWARE: pc\_sbo\_genes Version 1.0

/ SEQ ID NO 688

/ LENGTH: 915

/ TYPE: DNA  
/ ORGANISM: Homo sapiens

US-10-821-234-688

Query Match 6.0%; Score 59; DB 8; Length 915;  
Best Local Similarity 52.7%; Pred. No. 0.0097;  
Matches 128; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 500 TCCATCATTTTGTCTGACGTCAGTCAAGAGAGAGGAGTGGAGTCTGCGCAATGTGACTGCTCA 559

DB 639 TCCCTCAAGTGTCTCTCACTCCAGCAGACAGAGATTTGTCTGCGCAATGTGAGACAGATT 698

QY 560 TTATTTATCCAGATACAGATCAGACCTGTGATCTTCACTTACTGCTGTGAGGAA 619

DB 699 CTACTACATTCAGTCATTCATGGAATGCGCCCATTTAGTACAGTGATGTGGGGGAAA 758

QY 630 TGACATTAATCTTTGTAGAGGAGAGATTGCAAGCTGATGTGCAAAAGCTTTGAAAA 679

DB 759 TGAATAACAATTTACTCTCCAAACAGAAATGTGAGGGGATCTTAAAAAGGTTTCATCCA 818

QY 680 GAAAAGAAGATGCCAAGCTTGTGCTTGCAGTGAATCCGAAATTCGGAGAAGCA 739

DB 819 AAGATATCAAAAGAGGCTTATTTAAAAACAAAAGAAAAGAGAGAGAGTGA 878

QY 740 ATT 742

DB 879 AAT 881

RESULT 6  
US-11-000-463-214

/ Sequence 214, Application US/11000463  
/ Publication No. US20050266423A1

GENERAL INFORMATION:

/ APPLICANT: Tang, Y. Tom  
/ APPLICANT: Liu, Chenghua  
/ APPLICANT: Asundi, Vinod  
/ APPLICANT: Chen, Rui-hong  
/ APPLICANT: Qian, Xiaohong B.  
/ APPLICANT: Wang, Zhiwei  
/ APPLICANT: Wehrman, Tom  
/ APPLICANT: Zhou, Jie  
/ APPLICANT: Cao, Yi-Cheng

/ APPLICANT: Drmanac, Radjoje T.

/ TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides

/ FILE REFERENCE: 785CIPACN

/ CURRENT APPLICATION NUMBER: US/11/000,463

/ PRIOR FILING DATE: 2004-11-29

/ PRIOR APPLICATION NUMBER: 10/291,265

/ PRIOR FILING DATE: 2002-11-08

/ PRIOR APPLICATION NUMBER: PCT/US01/02623

/ PRIOR FILING DATE: 2001-01-25

/ PRIOR APPLICATION NUMBER: 09/922,279

/ PRIOR FILING DATE: 2001-08-03

/ PRIOR APPLICATION NUMBER: 09/491,404

/ PRIOR FILING DATE: 2000-01-25

/ PRIOR APPLICATION NUMBER: 09/617,746

/ PRIOR FILING DATE: 2000-07-17

/ PRIOR APPLICATION NUMBER: 09/631,451

/ PRIOR FILING DATE: 2000-08-03

/ PRIOR APPLICATION NUMBER: 09/633,870

/ PRIOR FILING DATE: 2000-09-15

/ NUMBER OF SEQ ID NOS: 944

/ SOFTWARE: FastSeq for Windows Version 3.0

/ SEQ ID NO 214

/ LENGTH: 1280

/ TYPE: DNA

/ ORGANISM: Homo sapiens

/ FEATURE: CDS

/ LOCATION: (103)..(1158)

US-11-000-463-214

Query Match 5.8%; Score 56.8; DB 12; Length 1280;

Best Local Similarity 59.1%; Pred. No. 0.0035;

Matches 97; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 135 GCGAGATCTGTCTCTGCCCCCTAGACTACAGACCTTCGCGGCCCTACTTCTCGCTTAC 194

DB 952 GTGGGGGCTTCATCTCCATCTCCATGATCTCGGGGCCCTTCGAGCTTATCATGCTCTGG 1011

QY 195 TACTACGACAGTACAGCAGAGCTGCGCCAGTTCCTGTACGGGGGCTGCGAGGGCAAC 254

DB 1012 GCATTGATGCTGTCAAGGAGAGTGCCTCTTCCCTACGGGGGCTGCGAGGGCAAC 1071

QY 255 GCCAACAATTTCTACACCTGAGAGGCTTGCAGACGATGCTTCTG 298

DB 1072 GGAACAAGTCTTACTCAGAGAAGAGTGCAGAGATGACTCGGG 1115

RESULT 7  
US-11-177-506-2

/ Sequence 2, Application US/11177506  
/ Publication No. US20060029956A1

GENERAL INFORMATION:

/ APPLICANT: Beyer, Wayne F.

/ APPLICANT: Venetta, Thomas M.

/ APPLICANT: Groelke, John W.

/ APPLICANT: Blasius, Rainer H.

/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE

/ FILE REFERENCE: 46143/294851

/ CURRENT APPLICATION NUMBER: US/11/177,506

/ PRIOR FILING DATE: 2005-07-08

/ PRIOR APPLICATION NUMBER: 60/586,856

/ PRIOR FILING DATE: 2004-07-09

/ NUMBER OF SEQ ID NOS: 52

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 2

/ LENGTH: 1413

/ TYPE: DNA

/ ORGANISM: Homo sapiens

/ NAME/KEY: CDS

/ LOCATION: (227)...(1285)

US-11-177-506-2

Query Match 5.8%; Score 56.8; DB 9; Length 1413;

Best Local Similarity 59.1%; Pred. No. 0.0036;

Matches 97; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 135 GCGAGATCTGTCTCTGCCCCCTAGACTACAGACCTTCGCGGCCCTACTTCTCGCTTAC 194

Db 1076 GTGGCGGCTGCAATCTCCCATATGTCGGGGCCCTGCCAGCTTATCCAGCTCTGG 1135  
Qy 195 TACTACGACAGGTATACGCGAGAGCTGCCGCAATTCCTGTACGCGGGCTGCCAGGGCAAC 254  
Db 1136 GCATTGTGCTGTACAGGGGGAAGTGCCTCTTCCCTTACGCGGGCTGCCAGGGCAAC 1195  
Qy 255 GCCAACATTTCTTACACCTGGGAGGCTTCCGACGATGCTTGGT 298  
Db 1196 GGAAACAAGTTCTACTCAGAGAAAGATGTCAGAGATCTGCGG 1239

## RESULT 8

US-11-000-463-686  
; Sequence 686, Application US/11000463  
; Publication No. US20050266423A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Qian, Xiaohong B.  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Zhang, Jie  
; APPLICANT: Zhou, Ping  
; APPLICANT: Cao, Yi-Cheng  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
; FILE REFERENCE: 785CIPACN  
; CURRENT APPLICATION NUMBER: US/11/000,463  
; PRIOR FILING DATE: 2004-11-29  
; PRIOR APPLICATION NUMBER: 10/291,265  
; PRIOR FILING DATE: 2002-11-08  
; PRIOR APPLICATION NUMBER: PCT/US01/02623  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 09/922,279  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: 09/491,404  
; PRIOR FILING DATE: 2000-01-25  
; PRIOR APPLICATION NUMBER: 09/617,746  
; PRIOR FILING DATE: 2000-07-17  
; PRIOR APPLICATION NUMBER: 09/631,451  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: 09/633,870  
; NUMBER OF SEQ ID NOS: 944  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 686  
; LENGTH: 1464  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-000-463-686

Query Match 5.8%; Score 56.8; DB 12; Length 1464;  
Best Local Similarity 59.1%; Pred. No. 0.0036;  
Matches 97; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Qy 135 GCGAGATCTGTCTCTCCCTAGACTACGAGACCTTCCGGCCCTTACTTCTCCGTAC 194  
Db 1137 GTGGGGGCTGCAATCTCCCATATGTCGGGGCCCTGCCAGCTTATCCAGCTCTGG 1196  
Qy 195 TACTACGACAGGTATACGCGAGAGCTGCCGCAATTCCTGTACGCGGGCTGCCAGGGCAAC 254  
Db 1197 GCATTGTGCTGTACAGGGGGAAGTGCCTCTTCCCTTACGCGGGCTGCCAGGGCAAC 1256  
Qy 255 GCCAACATTTCTTACACCTGGGAGGCTTCCGACGATGCTTGGT 298  
Db 1257 GGAAACAAGTTCTACTCAGAGAAAGATGTCAGAGATCTGCGG 1300

RESULT 9  
US-11-128-061-869  
; Sequence 869, Application US/11128061

; Publication No. US20060003958A1  
; GENERAL INFORMATION:  
; APPLICANT: Melville, Mark W.  
; APPLICANT: Charlebois, Timothy S.  
; APPLICANT: Mounts, William M.  
; APPLICANT: Hann, Louane E.  
; APPLICANT: Sinacore, Martin S.  
; APPLICANT: Leonard, Mark W.  
; APPLICANT: Brown, Eugene L.  
; APPLICANT: Miller, Christopher P.  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS  
; FILE REFERENCE: 01997.027701  
; CURRENT APPLICATION NUMBER: US/11/128,061  
; PRIOR FILING DATE: 2005-05-11  
; PRIOR APPLICATION NUMBER: US 60/570,425  
; NUMBER OF SEQ ID NOS: 7285  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 869  
; LENGTH: 1234  
; TYPE: DNA  
; ORGANISM: Mesocricetus auratus  
; FEATURES:  
; NAME/KEY: misc.feature  
; LOCATION: (876)..(891)  
; OTHER INFORMATION: n is a, c, g, or t  
US-11-128-061-869

Query Match 5.4%; Score 52.6; DB 12; Length 1234;  
Best Local Similarity 56.7%; Pred. No. 0.031;  
Matches 97; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

Qy 119 GCCAACAGGAATATACGCGAGATCTCTCCCTAGACTACGAGACCTTCCGGGCG 178  
Db 915 GCACGTCGGCGGACCGTAGGCGCTGCAATCTCCCATATCCAGGTCCCTGCCGTGC 974  
Qy 179 CCTACTTCTCGTTACTACTACGACAGGTACACGAGCTGCCGCAATTCCTGTACGG 238  
Db 975 CTAGTCGAGCTTGGGCAATTCGATGACGACAGGAAGATGCTCCAGTTCAGTTATGG 1034  
Qy 239 GGGCTGCGAGGGCAAGCCCAATTTCTTACCTTGGAGGCTTGGCAGCA 289  
Db 1035 CGGCTGCAAGGCAACGCGCAAGTTCTACTCCGAAAGAGTGCAGGA 1085

## RESULT 10

US-11-128-061-4511  
; Sequence 4511, Application US/11128061  
; Publication No. US2006003958A1  
; GENERAL INFORMATION:  
; APPLICANT: Melville, Mark W.  
; APPLICANT: Charlebois, Timothy S.  
; APPLICANT: Mounts, William M.  
; APPLICANT: Hann, Louane E.  
; APPLICANT: Sinacore, Martin S.  
; APPLICANT: Leonard, Mark W.  
; APPLICANT: Brown, Eugene L.  
; APPLICANT: Miller, Christopher P.  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS  
; FILE REFERENCE: 01997.027701  
; CURRENT APPLICATION NUMBER: US/11/128,061  
; PRIOR FILING DATE: 2005-05-11  
; PRIOR APPLICATION NUMBER: US 60/570,425  
; NUMBER OF SEQ ID NOS: 7285  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 4511  
; LENGTH: 1234  
; TYPE: DNA  
; ORGANISM: Mesocricetus auratus  
; FEATURES:

NAME/KEY: misc feature  
LOCATION: (8761..(891)  
OTHER INFORMATION: n is a, c, g, or t  
US-11-128-061-4511

Query Match 5.4%; Score 52.6; DB 12; Length 1234;  
Best Local Similarity 56.7%; Pred. No. 0.031;  
Matches 97; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 119 GCCAAGGAAATTAACGGGAGATCTGCTCTGCCCCCTAGACTAGGACCTGCGGCGC 178  
DB 915 GCAAGCGGCGGACCGTAGGCGGCTGCGAGTCTCCCAATAGCCAAAGGCTCCGCGCGC 974  
QY 179 CCTACTTCCGTTACTACTAGAGGTACAGGAGCGAGCGCGCGCGCGCTTCTGTACGG 238  
DB 975 CTACCTCAGCTCTGGGCAATTCGATGACGACAGGAGAAATGCTCCAGTTCAATTATGG 1034  
QY 239 GGGCTGCGAGGCGCAACCAATTTCTACACCTGGAGGCTTCCGACGA 289  
DB 1035 CGGCTGCAAGGCAACGGCAACAACTTCTACTCCGAGAGAGAGTCAAGGA 1085

## RESULT 11

US-11-128-049-869  
Sequence 869, Application US/11128049  
Publication No. US20060010513A1  
GENERAL INFORMATION:  
APPLICANT: Melville, Mark W.  
APPLICANT: Charlebois, Timothy S.  
APPLICANT: Mounts, William M.  
APPLICANT: Ham, Louane B.  
APPLICANT: Sinacore, Martin S.  
APPLICANT: Leonard, Mark W.  
APPLICANT: Brown, Eugene L.  
APPLICANT: Miller, Christopher P.  
TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR  
TITLE OF INVENTION: MAKING AND USING SAME  
FILE REFERENCE: 01997.027700  
CURRENT APPLICATION NUMBER: US/11/128,049  
CURRENT FILING DATE: 2005-05-11  
PRIOR APPLICATION NUMBER: US 60/570,425  
PRIOR FILING DATE: 2004-05-11  
NUMBER OF SEQ ID NOS: 7285  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 869  
LENGTH: 1234  
TYPE: DNA  
ORGANISM: Mesocricetus auratus  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (8761..(891)  
OTHER INFORMATION: n is a, c, g, or t  
US-11-128-049-869

Query Match 5.4%; Score 52.6; DB 12; Length 1234;  
Best Local Similarity 56.7%; Pred. No. 0.031;  
Matches 97; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 119 GCCAAGGAAATTAACGGGAGATCTGCTCTGCCCCCTAGACTAGGACCTGCGGCGC 178  
DB 915 GCAAGCGGCGGACCGTAGGCGGCTGCGAGTCTCCCAATAGCCAAAGGCTCCGCGCGC 974  
QY 179 CCTACTTCCGTTACTACTAGAGGTACAGGAGCGAGCGCGCGCGCTTCTGTACGG 238  
DB 975 CTACCTCAGCTCTGGGCAATTCGATGACGACAGGAGAAATGCTCCAGTTCAATTATGG 1034  
QY 239 GGGCTGCGAGGCGCAACCAATTTCTACACCTGGAGGCTTCCGACGA 289  
DB 1035 CGGCTGCAAGGCAACGGCAACAACTTCTACTCCGAGAGAGAGTCAAGGA 1085

RESULT 12  
US-11-128-049-4511

Sequence 4511, Application US/11128049  
Publication No. US20060010513A1  
GENERAL INFORMATION:

APPLICANT: Melville, Mark W.  
APPLICANT: Charlebois, Timothy S.  
APPLICANT: Mounts, William M.  
APPLICANT: Ham, Louane B.  
APPLICANT: Sinacore, Martin S.  
APPLICANT: Leonard, Mark W.  
APPLICANT: Brown, Eugene L.  
APPLICANT: Miller, Christopher P.  
TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR  
TITLE OF INVENTION: MAKING AND USING SAME  
FILE REFERENCE: 01997.027700  
CURRENT APPLICATION NUMBER: US/11/128,049  
CURRENT FILING DATE: 2005-05-11  
PRIOR APPLICATION NUMBER: US 60/570,425  
PRIOR FILING DATE: 2004-05-11  
NUMBER OF SEQ ID NOS: 7285  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 4511  
LENGTH: 1234  
TYPE: DNA  
ORGANISM: Mesocricetus auratus  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (8761..(891)  
OTHER INFORMATION: n is a, c, g, or t  
US-11-128-049-4511

Query Match 5.4%; Score 52.6; DB 12; Length 1234;  
Best Local Similarity 56.7%; Pred. No. 0.031;  
Matches 97; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 119 GCCAAGGAAATTAACGGGAGATCTGCTCTGCCCCCTAGACTAGGACCTGCGGCGC 178  
DB 915 GCAAGCGGCGGACCGTAGGCGGCTGCGAGTCTCCCAATAGCCAAAGGCTCCGCGCGC 974  
QY 179 CCTACTTCCGTTACTACTAGAGGTACAGGAGCGAGCGCGCGCGCTTCTGTACGG 238  
DB 975 CTACCTCAGCTCTGGGCAATTCGATGACGACAGGAGAAATGCTCCAGTTCAATTATGG 1034  
QY 239 GGGCTGCGAGGCGCAACCAATTTCTACACCTGGAGGCTTCCGACGA 289  
DB 1035 CGGCTGCAAGGCAACGGCAACAACTTCTACTCCGAGAGAGAGTCAAGGA 1085

## RESULT 13

US-11-128-061-6860  
Sequence 6860, Application US/11128061  
Publication No. US2006003958A1  
GENERAL INFORMATION:  
APPLICANT: Melville, Mark W.  
APPLICANT: Charlebois, Timothy S.  
APPLICANT: Mounts, William M.  
APPLICANT: Ham, Louane B.  
APPLICANT: Sinacore, Martin S.  
APPLICANT: Leonard, Mark W.  
APPLICANT: Brown, Eugene L.  
APPLICANT: Miller, Christopher P.  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS  
TITLE OF INVENTION: TO MONITOR GENE EXPRESSION  
FILE REFERENCE: 01997.027701  
CURRENT APPLICATION NUMBER: US/11/128,061  
CURRENT FILING DATE: 2005-05-11  
PRIOR APPLICATION NUMBER: US 60/570,425  
PRIOR FILING DATE: 2004-05-11  
NUMBER OF SEQ ID NOS: 7285  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 6860  
LENGTH: 600  
TYPE: DNA  
ORGANISM: Cricetus griseus

US-11-128-061-6860

Query Match 5.3%; Score 52; DB 12; Length 600;  
 Best Local Similarity 55.6%; Pred. No. 0.033;  
 Matches 100; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 505 CATTTTGCTACAGTCCAAAAGATGAGGAGCTGTGCTCTGCCAATGTGACTCGCTATTATT 564  
 |||||  
 DB 225 CATTTGGCCCAATGAAGGTAGATGATGACCGTGCAAAACCATGATGAAGAGTTATTTT 284  
 |||||  
 QY 565 TTAATCCAAAGATACAGAACCTGTGATCTTTCACCTATCTGCTGTGAGGGAATGACA 624  
 |||||  
 DB 285 TCAATATTTTACTTACCAATGTGAAGATTATATATGGGGATGCAGAGAAACGAAA 344  
 |||||  
 QY 625 ATAACTTTGTAGAGGAGATGTCGCAACGTGCATGTGCAAAAGCTTTGAAAAAGAAA 684  
 |||||  
 DB 345 ATCGATTTGAAACCTGGAGAGATGTAAAGAGACATGCATCAGAGGTTATTAAGAAAGA 404  
 |||||

RESULT 14

US-11-128-049-6860  
 ; Sequence 6860, Application US/11128049  
 ; Publication No. US20060010513A1  
 ; GENERAL INFORMATION:

; APPLICANT: Melville, Mark W.  
 ; APPLICANT: Charlebois, Timothy S.  
 ; APPLICANT: Mounts, William M.  
 ; APPLICANT: Hann, Louane E.  
 ; APPLICANT: Sinacore, Martin S.  
 ; APPLICANT: Leonard, Mark W.  
 ; APPLICANT: Brown, Eugene L.  
 ; APPLICANT: Miller, Christopher P.  
 ; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR  
 ; FILE REFERENCE: 01997.027700  
 ; CURRENT APPLICATION NUMBER: US/11/128,049  
 ; PRIOR FILING DATE: 2005-05-11  
 ; PRIOR APPLICATION NUMBER: US 60/570,425  
 ; NUMBER OF SEQ ID NOS: 7285  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 6860  
 ; LENGTH: 600  
 ; TYPE: DNA  
 ; ORGANISM: Cricetus griseus  
 ; ORGANISM: Cricetus griseus  
 ; US-11-128-049-6860

Query Match 5.3%; Score 52; DB 12; Length 600;  
 Best Local Similarity 55.6%; Pred. No. 0.033;  
 Matches 100; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 505 CATTTTGCTACAGTCCAAAAGATGAGGAGCTGTGCTCTGCCAATGTGACTCGCTATTATT 564  
 |||||  
 DB 225 CATTTGGCCCAATGAAGGTAGATGATGACCGTGCAAAACCATGATGAAGAGTTATTTT 284  
 |||||  
 QY 565 TTAATCCAAAGATACAGAACCTGTGATCTTTCACCTATCTGCTGTGAGGGAATGACA 624  
 |||||  
 DB 285 TCAATATTTTACTTACCAATGTGAAGATTATATATGGGGATGCAGAGAAACGAAA 344  
 |||||  
 QY 625 ATAACTTTGTAGAGGAGATGTCGCAACGTGCATGTGCAAAAGCTTTGAAAAAGAAA 684  
 |||||  
 DB 345 ATCGATTTGAAACCTGGAGAGATGTAAAGAGACATGCATCAGAGGTTATTAAGAAAGA 404  
 |||||

RESULT 15

US-11-128-061-3218  
 ; Sequence 3218, Application US/11128061  
 ; Publication No. US20060003958A1  
 ; GENERAL INFORMATION:

; APPLICANT: Melville, Mark W.  
 ; APPLICANT: Charlebois, Timothy S.  
 ; APPLICANT: Mounts, William M.  
 ; APPLICANT: Hann, Louane E.

; APPLICANT: Sinacore, Martin S.  
 ; APPLICANT: Leonard, Mark W.  
 ; APPLICANT: Brown, Eugene L.  
 ; APPLICANT: Miller, Christopher P.  
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS  
 ; FILE REFERENCE: 01997.027701  
 ; CURRENT APPLICATION NUMBER: US/11/128,061  
 ; PRIOR FILING DATE: 2005-05-11  
 ; PRIOR APPLICATION NUMBER: US 60/570,425  
 ; NUMBER OF SEQ ID NOS: 7285  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 3218  
 ; LENGTH: 650  
 ; TYPE: DNA  
 ; ORGANISM: Cricetus griseus  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)..(21)  
 ; OTHER INFORMATION: n is a, c, g, or t  
 ; US-11-128-061-3218

Query Match 5.3%; Score 52; DB 12; Length 650;  
 Best Local Similarity 55.6%; Pred. No. 0.033;  
 Matches 100; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 505 CATTTTGCTACAGTCCAAAAGATGAGGAGCTGTGCTCTGCCAATGTGACTCGCTATTATT 564  
 |||||  
 DB 275 CATTTGGCCCAATGAAGGTAGATGATGACCGTGCAAAACCATGATGAAGAGTTATTTT 334  
 |||||  
 QY 565 TTAATCCAAAGATACAGAACCTGTGATCTTTCACCTATCTGCTGTGAGGGAATGACA 624  
 |||||  
 DB 335 TCAATATTTTACTTACCAATGTGAAGATTATATATGGGGATGCAGAGAAACGAAA 394  
 |||||  
 QY 625 ATAACTTTGTAGAGGAGATGTCGCAACGTGCATGTGCAAAAGCTTTGAAAAAGAAA 684  
 |||||  
 DB 395 ATCGATTTGAAACCTGGAGAGATGTAAAGAGACATGCATCAGAGGTTATTAAGAAAGA 454  
 |||||

Search completed: March 11, 2006, 06:32:19  
 Job time : 438 secs